

From: Chan, Christina
Sent: Friday, October 28, 2005 3:07 PM
To: Basi, Nirmal; STIC-Biotech/ChemLib
Subject: RE: Rush search for 09/823,069

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
OCT 28 2005
ECH/OIEN DIVISION
(STIC)

-----Original Message-----

From: Basi, Nirmal
Sent: Friday, October 28, 2005 3:01 PM
To: Chan, Christina
Subject: Rush search for 09/823,069

Christina I am seeking approval for a RUSH sequence search for an Amended case, as indicated below. If approved, could you please forward the search to STIC and cc a copy to me.

Examiner: Nirmal S. Basi
Art Unit 1646
Office: Remsen Building, Room 4D68
Mail Room: Remsen Building, room 4C70

Sequence search:

App. #: 09/823,069

Result format: Paper.

Title: **METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE VARIANT OF THE SIGMA-1 RECEPTOR**

206 1-579 NA
2-192 AA

Inventors: Wheeler, Kenneth

Priority Date: 4/3/2000

Please search:

i) SEQ ID NOs: 1 and 2

10/31/05
JTH

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

Date completed:	Search Site	Vendors
Searcher: <u>Beverly e 2528</u>	<input type="checkbox"/> STIC	<input type="checkbox"/> IG
Terminal time: _____	<input type="checkbox"/> CM-1	<input type="checkbox"/> STN
Elapsed time: _____	<input type="checkbox"/> Pre-S	<input type="checkbox"/> Dialog
CPU time: _____	Type of Search	<input type="checkbox"/> APS
Total time: _____	<input type="checkbox"/> N.A. Sequence	<input type="checkbox"/> Geninfo
Number of Searches: _____	<input type="checkbox"/> A.A. Sequence	<input type="checkbox"/> SDC
Number of Databases: _____	<input type="checkbox"/> Structure	<input type="checkbox"/> DARC/Questel
	<input type="checkbox"/> Bibliographic	<input checked="" type="checkbox"/> Other <u>CGN</u>

TO-1560 (9-90)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 29, 2005, 04:28:43 ; Search time 176 Seconds
(without alignments)
558.632 Million cell updates/sec

Title: US-09-823-069A-2
Perfect score: 1016
Sequence: 1 MQWAVGRRWAWAALLAVAA.....RSVARGRLLELTTLFGQDP 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues 1612378

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1016	100.0	192	Q9NYX0	Q9NYX0 homo sapien
2	990.5	97.5	223	Q99720	Q99720 homo sapien
3	940.5	92.6	223	Q9ROC9	Q9ROC9 rattus norv
4	934.5	92.0	223	Q9Z2W2	Q9Z2W2 rattus norv
5	925	91.0	192	Q9JKU9	Q9JKU9 mus musculu
6	918.5	90.4	223	Q60492	Q60492 cavia porce
7	903.5	88.9	223	O55242	O55242 mus musculu
8	767.5	75.5	187	Q8N7H3	Q8N7H3 homo sapien
9	636.5	62.6	221	Q6DCU6	Q6DCU6 xenopus lae
10	631.5	62.2	223	Q645J3	Q645J3 taricha gra
11	629.5	62.0	221	Q661M1	Q661M1 xenopus tro
12	616.5	60.7	222	Q7ZMG9	Q7ZMG9 brachydanio
13	544	53.5	106	Q7Z653	Q7Z653 homo sapien
14	508	50.0	106	Q9RLJ7	Q9RLJ7 rattus norv
15	228.5	22.5	256	Q9C2G3	Q9C2G3 neurospora
16	227	22.3	224	Q6FKL1	Q6FKL1 candida gla
17	226.5	22.3	256	1 ERG2 NEUCR	Q92254 neurospora
18	224	22.0	217	Q6BSC9	Q6BSC9 debatyomyce
19	218	21.5	223	Q6CL22	Q6CL22 kluyveromyc
20	217.5	21.4	218	Q6C3U4	Q6C3U4 yarrowia li
21	214.5	21.1	218	Q6CEA6	Q6CEA6 yarrowia li
22	212.5	20.9	222	1 ERG2 YEAST	P32352 saccharomyc
23	211	20.8	222	Q755O1	Q755Q1 ashbya goss
24	210.5	20.7	221	1 ERG2 MAGGR	P33281 magnaporthe
25	206	20.3	219	1 ERG2 SCHPO	P87113 schizosacch
26	204	20.1	285	2 Q7RVD2	Q7RVD2 neurospora
27	183.5	18.1	241	1 ERG2 USTMA	P32360 ustilago ma
28	94	9.3	393	2 Q9ZVZ4	Q9ZVZ4 arabidopsis
29	94	9.3	527	2 Q6GM93	Q6GM93 xenopus lae
30	93	9.2	397	2 Q8PIU1	Q8PIU1 xanthomonas
31	93	9.2	417	2 Q7NSI9	Q7NSI9 chromobacte

ALIGNMENTS

RESULT 1

Q9NYX0 PRELIMINARY; PRT; 192 AA.
AC Q9NYX0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Sigma 1 receptor beta variant.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Wang L.-M., Shelness G.S., Childers S.R., Mach R.H., Wheeler K.T.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
EMBL: AF226604; AAF64280.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:000247; F:C-8 sterol isomerase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006696; P:ergosterol biosynthesis; IEA.
DR InterPro; IPR006716; ERG2_Sireceptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.
KW Receptor.
SQ SEQUENCE 192 AA; 21483 MW; 9E0C6A120A89126F CRC64;

Query Match 100.0%; Score 1016; DB 2; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.4e-84;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQWAVGRRWAWAALLAVAAVLTVVWLVLTQSFVQREIEIAQLARQYAGLDHDLAFSR 60
DB 1 MQWAVGRRWAWAALLAVAAVLTVVWLVLTQSFVQREIEIAQLARQYAGLDHDLAFSR 60
QY 61 LIVELRLPHGHVLPDEELQWVFVNAVAGGMWGANCLLHASLSEYVLLFGTALGRHSGET 120
DB 61 LIVELRLPHGHVLPDEELQWVFVNAVAGGMWGANCLLHASLSEYVLLFGTALGRHSGET 120
QY 121 VHGPGEATAVWGPNVTWVEYGRGVIPSTLAFALADTVFSTODFLTPVTLRSYARGLR 180
DB 121 VHGPGEATAVWGPNVTWVEYGRGVIPSTLAFALADTVFSTODFLTPVTLRSYARGLR 180
QY 181 LEITTVLFGQDP 192
DB 181 LEITTVLFGQDP 192
RESULT 2
Q99720 PRELIMINARY; PRT; 223 AA.
AC Q99720; O00673; O00725;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)

DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Type I sigma receptor (Opioid receptor, sigma 1, isoform 1) (SR31747)
DE binding protein 1) (OPRS1 protein).
GN Name=OPRS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Chorion; Chorion;
RX MEDLINE=97127440; PubMed=8954936; DOI=10.1006/bbrc.1996.1842;
RA Kerkut R., Prasad P.D., Fei Y.J., Leibach F.H., Ganapathy V.;
RT "Cloning and functional expression of the human type I sigma receptor
RT (hSigmaR1).";
RL Biochem. Biophys. Res. Commun. 229:553-558 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98114282; PubMed=9453537;
RA Prasad P.D., Li H.W., Fei Y.J., Ganapathy M.E., Fujita T.,
RA Plumley L.H., Yang-Feng T.L., Leibach F.H., Ganapathy V.;
RT "Exon-intron structure, analysis of promoter region, and chromosomal
RT localization of the human type I sigma receptor gene.";
RL J. Neurochem. 70:443-451 (1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deng J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Casillas P., Jbilo O., Vidal H.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; U75283; AAB50402.1; -;
DR EMBL; AF001977; AAC04507.1; -;
DR EMBL; AF001976; AAC04507.1; JOINED.
DR EMBL; BC004899; AAB04899.1; -;
DR EMBL; U79528; AAB51238.1; -;
DR EMBL; CR457075; CAG33356.1; -;
DR PIR; JCS266; JCS266.
DR Genew; HGNC:8157; OPRS1.
DR GO; GO:0005887; C-integral to plasma membrane; TAS.
DR GO; GO:0008144; F-drug binding; TAS.
DR InterPro; IPR006716; ERG2_Sireceptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.

KW Receptor.
SQ SEQUENCE 223 AA; 25128 MW; 0C498636BEB1C443 CRC64;
Query Match 97.5%; Score 990.5; DB 2; Length 223;
Best Local Similarity 86.1%; Pred. No. 5.9e-82;
Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
QY 1 MQWAVGRWAAALLLAAVAVLTQVWLWLTQTSQVFOREIAQLARQVAGLDHLEAFSR 60
DB 1 MQWAVGRWAAALLLAAVAVLTQVWLWLTQTSQVFOREIAQLARQVAGLDHLEAFSR 60
QY 61 LIVLRLRLHPGHVLPDEELQWVFNAGGWMGAMCILLHASLSEYVLLFTGLSGRHS--- 117
DB 61 LIVLRLRLHPGHVLPDEELQWVFNAGGWMGAMCILLHASLSEYVLLFTGLSGRHSGRY 120
QY 118 -----GETTVVHGPGGATAVEMGPNMTVMVEYGRGVIPS 149
DB 121 WAEISDTTIISGTFHQWREGTTKSEVFYFGPGGATAVEMGPNMTVMVEYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFLTFLYTLRSYARGRLRLTYLFGQDP 192
DB 181 TLAFALADTVFSTQDFLTFLYTLRSYARGRLRLTYLFGQDP 223
RESULT 3
Q9ROC9 PRELIMINARY; PRT; 223 AA.
AC Q9ROC9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Signal receptor (Opioid receptor, sigma 1).
GN Name=OPRS1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Mei J., Pasternak G.W.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Deng J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067769; AAF08342.1; -;
DR EMBL; BC061978; AAB61978.1; -;

DR GO:0005783; C-endoplasmic reticulum; IEA.
 DR GO:0000247; F-C-8 sterol isomerase activity; IEA.
 DR GO:0004872; F-receptor activity; IEA.
 DR GO:0006696; P-ergosterol biosynthesis; IEA.
 DR InterPro:IPR006716; ERG2_Sireceptlik.
 DR Pfam:PF04622; ERG2_SigmaIR; 1.
 KW Receptor.
 SQ SEQUENCE 223 AA; 25270 MW; B125A0388F1FFC6E CRC64;
 Query Match 92.6%; Score 940.5; DB 2; Length 223;
 Best Local Similarity 80.3%; Pred. No. 2.1e-77;
 Matches 179; Conservative 4; Mismatches 9; Indels 31; Gaps 1;
 QY 1 MOWAVGRRWAAALLAVAVLTQVWMLGTQSFVFORBEEIAQLARQYAGLDHLEAFSR 60
 DB 1 MPWAVGRRWAWITLFTIVAVLIQAVWMLGTQSFVFORBEEIAQLARQYAGLDHLEAFSR 60
 QY 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALSGRHS --- 117
 DB 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALSGHSGRY 120
 QY 118 -----GETVHGPGEATAVWGPNNTWVVEYGRGVIPS 149
 DB 121 WAEISDTIISGTFHQWREGTTKSEVYYPGETVHGPGEATAVWGPNNTWVVEYGRGVIPS 180
 QY 150 TLAFALADTVFSTQDFTLTYTLRSYARGRLRLLELTLYLFGQDP 192
 DB 181 TLAFALSDTIFSTQDFTLTYTLRSYARGRLRLLELTLYLFGQDP 223
 RESULT 4
 Q922W2 PRELIMINARY; PRT; 223 AA.
 AC Q922W2;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Brain sigma receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=98149355; PubMed=9489711;
 RA Seth P., Fei Y.-J., Li H.W., Huang W., Leibach F.H., Ganapathy V.;
 RT "Cloning and functional characterization of a sigma receptor from rat
 RT brain.";
 RL J. Neurochem. 70:922-931(1998).
 DR EMBL; AF004218; AAD01198.1; -;
 DR GO:0005783; C-endoplasmic reticulum; IEA.
 DR GO:0000247; F-C-8 sterol isomerase activity; IEA.
 DR GO:0004872; F-receptor activity; IEA.
 DR GO:0006696; P-ergosterol biosynthesis; IEA.
 DR InterPro:IPR006716; ERG2_Sireceptlik.
 DR Pfam:PF04622; ERG2_SigmaIR; 1.
 KW Receptor.
 SQ SEQUENCE 223 AA; 25314 MW; B122D7488F1FF96B CRC64;
 Query Match 92.08; Score 934.5; DB 2; Length 223;
 Best Local Similarity 79.8%; Pred. No. 7.3e-77;
 Matches 178; Conservative 4; Mismatches 10; Indels 31; Gaps 1;
 QY 1 MOWAVGRRWAAALLAVAVLTQVWMLGTQSFVFORBEEIAQLARQYAGLDHLEAFSR 60
 DB 1 MPWAVGRRWAWITLFTIVAVLIQAVWMLGTQSFVFORBEEIAQLARQYAGLDHLEAFSR 60
 QY 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALSGRHS --- 117
 DB 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALSGHSGRY 120
 QY 118 -----GETVHGPGEATAVWGPNNTWVVEYGRGVIPS 149

DB 121 WAEISDTIISGTFHQWREGTTKSEVYYPGETVHGPGEATAVWGPNNTWVVEYGRGVIPS 180
 QY 150 TLAFALADTVFSTQDFTLTYTLRSYARGRLRLLELTLYLFGQDP 192
 DB 181 TLAFALSDTIFSTQDFTLTYTLRSYARGRLRLLELTLYLFGQDP 223
 RESULT 5
 Q9JKU9 PRELIMINARY; PRT; 192 AA.
 AC Q9JKU9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sigma 1 receptor beta variant.
 DE Mus musculus (Mouse)
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hej; TISSUE=Breast;
 RA Wang L.-W., Shelness G.S., Childers S.R., Mach R.H., Wheeler K.T.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF226605; AAF64281.1; -;
 DR GO:0005783; C-endoplasmic reticulum; IEA.
 DR GO:0000247; F-C-8 sterol isomerase activity; IEA.
 DR GO:0004872; F-receptor activity; IEA.
 DR GO:0006696; P-ergosterol biosynthesis; IEA.
 DR InterPro:IPR006716; ERG2_Sireceptlik.
 DR Pfam:PF04622; ERG2_SigmaIR; 1.
 KW Receptor.
 SQ SEQUENCE 192 AA; 21603 MW; 01B4D60BF446D3A9 CRC64;
 Query Match 91.0%; Score 925; DB 2; Length 192;
 Best Local Similarity 89.0%; Pred. No. 4.6e-76;
 Matches 170; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MOWAVGRRWAAALLAVAVLTQVWMLGTQSFVFORBEEIAQLARQYAGLDHLEAFSR 60
 DB 1 MPWAVGRRWAWITLFTIVAVLIQAVWMLGTQSFVFORBEEIAQLARQYAGLDHLEAFSR 60
 QY 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALSGRHSGET 120
 DB 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALSGHSGET 120
 QY 121 VVHGPGEATAVWGPNNTWVVEYGRGVIPSTLAFALADTVFSTQDFTLTYTLRSYARGLR 180
 DB 121 VVHGPGEATALEWGPNTWVVEYGRGVIPSTLFPALADTVFSTQDFTLTYTLRSYARGLR 180
 QY 181 LEITTYLFGQD 191
 DB 181 LEITTYLFGQD 191
 RESULT 6
 Q60492 PRELIMINARY; PRT; 223 AA.
 AC Q60492;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sigma1-receptor (Sterol-isomerase like protein).
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fairbright white; TISSUE=Liver;
 RX MEDLINE=96353947; PubMed=8755605; DOI=10.1073/pnas.93.15.8072;
 RA Hanner M., Moebius F.F., Flandorfer A., Knaus H.G., Striessenig J.,

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RA Kempner E., Glosemann H.;
RT "Purification, molecular cloning, and expression of the mammalian
RL signal-binding site.";
RL EMBL; 266537; CAA91441.1; -.
DR GO; GO:0005783; C-endoplasmic reticulum; IEA.
DR GO; GO:0000247; F-C-8 sterol isomerase activity; IEA.
DR GO; GO:0004685; F-isomerase activity; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:0006696; P-ergosterol biosynthesis; IEA.
DR InterPro; IPR006716; ERG2_S1receptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.
KW Isomerase; Receptor_SigmaIR; 1.
SQ SEQUENCE 223 AA; 25311 MW; 4115E51096D548F8 CRC64;

Query Match 90.4%; Score 918.5; DB 2; Length 223;
Best Local Similarity 79.4%; Pred. No. 2.1e-75;
Matches 177; Conservative 4; Mismatches 11; Indels 31; Gaps 1;

QY 1 MQWAVGRWAWAALLLAVALTQVWLWLTQSFVQFQREETAQLARQYAGLDHLEAFSR 60
DB 1 MQWAVGRWAWAALLLAVALTQVWLWLTQSFVQFQREETAQLARQYAGLDHLEAFSK 60

QY 61 LIVELRLRHPGVLPDEELQWVFNAGWGMGAMCLLHASLSYVLLFGTALGSRGHS--- 117
DB 61 LIVELRLRHPGVLPDEELQWVFNAGWGMGAMCLLHASLSYVLLFGTALGSRHSGRY 120

QY 118 -----GETVHVGPGGATAVWGPNMTVMVEYGRGVIPS 149
DB 121 WAEISDTIISGTFHQWKEGTTKSEFYPGGETVHVGPGGATAVWGPNMTVMVEYGRGVIPS 180

QY 150 TLAPALADTVSTQDFLFTYTLRSYARGRLRLTLYLFGQDP 192
DB 181 TLGFALADTVSTQDFLFTYTLRVYARALQELTLYLFGQDP 223

RESULT 7
OS5242
ID 055242 PRELIMINARY; PRT; 223 AA.
AC 055242;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Type 1 sigma receptor (Oprl protein) (Sigma 1 receptor).
GN Name=Oprl;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SV, and C57BL/6; TISSUE=Kidney;
RX MEDLINE=98086386; PubMed=9425306; DOI=10.1006/bbrc.1997.7840;
RA Seth P., Leibach F.H., Ganapathy V.;
RT "Cloning and structural analysis of the cDNA and the gene encoding the
RT murine type 1 sigma receptor.";
RL Biochem. Biophys. Res. Commun. 241:535-540(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N, and FVB/N;
RC TISSUE=Liver, and Mammary tumor. WAP-TGF alpha model. 7 months old;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=97419861; PubMed=9274937; DOI=10.1016/S0014-2999(97)01064-9;
RA King M., Pan Y.X., Mei J., Chang A., Xu J., Pasternak G.W.;
RT "Enhanced kappa-opioid receptor-mediated analgesia by antisense
RT targeting the sigma receptor.";
RL Eur. J. Pharmacol. 331:R5-R6(1997).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Pan Y.-X., Xu J., Mei J.F., King M., Cang A., Wan B.-L.,
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030199; AAB97683.1; -.
DR EMBL; BC002000; AAH02000.1; -.
DR EMBL; BC019930; AAH19930.1; -.
DR EMBL; AF004927; AAC33306.1; -.
DR EMBL; AF030198; AAC39951.1; -.
DR PIR; JC5815; JCS815.
DR MGD; MGI:1195268; Oprl.
DR GO; GO:0004872; F-receptor activity; IDA.
DR InterPro; IPR006716; ERG2_S1receptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.
KW Receptor.
SQ SEQUENCE 223 AA; 25250 MW; 54BB2F14472B3512 CRC64;

Query Match 88.9%; Score 903.5; DB 2; Length 223;
Best Local Similarity 77.0%; Pred. No. 4.8e-74;
Matches 171; Conservative 7; Mismatches 13; Indels 31; Gaps 1;

QY 1 MQWAVGRWAWAALLLAVALTQVWLWLTQSFVQFQREETAQLARQYAGLDHLEAFSR 60
DB 1 MPWAGRWAWITLITLITIAVLQIAWLTQNFVQFQREETAQLARQYAGLDHLEAFSR 60

QY 61 LIVELRLRHPGVLPDEELQWVFNAGWGMGAMCLLHASLSYVLLFGTALGSRGHS--- 117
DB 61 LIVELRLRHPGVLPDEELQWVFNAGWGMGAMCLLHASLSYVLLFGTALGSHSGRY 120

QY 118 -----GETVHVGPGGATAVWGPNMTVMVEYGRGVIPS 149
DB 121 WAEISDTIISGTFHQWKEGTTKSEFYPGGETVHVGPGGATAVWGPNMTVMVEYGRGVIPS 180

QY 150 TLAPALADTVSTQDFLFTYTLRSYARGRLRLTLYLFGQD 191
DB 181 TLGFALADTVSTQDFLFTYTLRAYARGRLRLTLYLFGQD 222

RESULT 8
Q8N7H3
ID Q8N7H3 PRELIMINARY; PRT; 187 AA.
AC Q8N7H3;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

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DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ25585.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA Katsuta N., Sato K., Tanikawa M., Yamazaki M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Osuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA Nagai K., Isogai T., Sugano S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK098451; BAC0307.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:000247; F:C-8 sterol isomerase activity; IEA.
DR GO; GO:004872; F:receptor activity; IEA.
DR GO; GO:000696; P:ergosterol biosynthesis; IEA.
DR InterPro; IPR006716; ERG2_Sireceptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.
KW Receptor.
SQ SEQUENCE 187 AA; 21013 MW; E50731B80FB98PBF CRC64;

Query Match 75.5%; Score 767.5; DB 2; Length 187;
Best Local Similarity 70.0%; Pred. No. 9.3e-62;
Matches 156; Conservative 0; Mismatches 0; Indels 67; Gaps 3;

QY 1 MOWAGRRWAWAALLAVAVLTQVVMVLTQSFVQREIAQLARQVAGLDHLEAFSR 60
DB 1 MOWAGRRWAWAALLAVAVLTQVVMVLTQSFVQREIAQLARQVAGLDHLEAFSR 38
|||
QY 61 LIVELRLHPGHVLPDEELQWVFNAGWGMAMCLLHSLSEYVLLFGTALGRGHS 117
DB 39 LI-----EELQWVFNAGWGMAMCLLHSLSEYVLLFGTALGRGHSGRY 84
|||
QY 118 -----GETVHVGGEATAVNGPNTVMVVEYGRGVIPS 149
DB 85 WABISDTISGTTFHQWREGTKSEVFYPGTETVHVGGEATAVNGPNTVMVVEYGRGVIPS 144
|||
QY 150 TLAFALADTVFSTQDFLTFLYTLRSYARGLRLELTLYLFGQDP 192
DB 145 TLAFALADTVFSTQDFLTFLYTLRSYARGLRLELTLYLFGQDP 187
|||

RESULT 9
Q6DCU6 PRELIMINARY; PRT; 221 AA.
AC Q6DCU6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Opre1-prov protein.
GN Name-oprs1-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shavchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC077894; AAH77894.1; -
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:000247; F:C-8 sterol isomerase activity; IEA.
DR GO; GO:000696; P:ergosterol biosynthesis; IEA.
DR InterPro; IPR006716; ERG2_Sireceptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.
SQ SEQUENCE 221 AA; 24695 MW; D0D9626B03D07EAE CRC64;

Query Match 62.6%; Score 636.5; DB 2; Length 221;
Best Local Similarity 58.0%; Pred. No. 9.1e-50;
Matches 120; Conservative 34; Mismatches 22; Indels 31; Gaps 1;

QY 12 AALLAVAAVLTQVVMVLTQSFVQREIAQLARQVAGLDHLEAFSLIVELRLHPG 71
DB 9 AVLWVAGLAVLQLTRGWLSSKSYFNREIARLAKHSGLDYEVAFSKIIVELRKHGP 68
|||
QY 72 HVLDPDEELQWVFNAGWGMAMCLLHSLSEYVLLFGTALGRGHS 117
DB 69 HILQDEDLQWVFNAGWGMAMCLLHSLSEYVLLFGTAVDTGHSRYWAEISDTLSG 128
|||
QY 118 -----GETVHVGGEATAVNGPNTVMVVEYGRGVIPSTLAFALADTVF 160
DB 129 TFRQWKEGTTKSEIFYPGDTIVHVEGATSVQWSSGTMVVEYGRGFIPSTLAFALADTVF 188
|||
QY 161 STQDFLTFLYTLRSYARGLRLELTLYL 187
DB 189 STQDFLTFLYTLRSYARGLRLELTLYL 215
|||

RESULT 10
Q645J3 PRELIMINARY; PRT; 223 AA.
AC Q645J3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Sigma receptor.
OS Taricha granulosa (Roughskin newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandridae; Salamandridae; Taricha.
OX NCBI_TaxID=8321;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Bradford C.S., Moore F.L.;
RT "Cloning, Expression, and Characterization of a Sigma Receptor from
RT the Brain of the Rough-skinned Newt, Taricha granulosa.";

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY726668; AAU34079.1; -.
KW Receptor.

Query Match	62.2%	Score 631.5	DB 2	Length 223
Best Local Similarity	57.5%	Pred. No. 2.6e-49		
Matches 119	Conservative 31	Mismatches 26	Indels 31	Gaps 1
Qy	12	AAULLAAVAALVTQVWLWLGTQSFVFOREETAAQLARQAVAGLDHELAFGRSLIVELRRLHPG	71	
Db	11	AAUGLAVLAVVQLLRTWLSSKSYLFNQKDIAELAKQHAGMDPEVAFSKIIVELKKHPG	70	
Qy	72	HVLPEELQWVFNAGGMGAMCLLHSLSEYVLLFGTALSGRHSS	117	
Db	71	HILPDEDLQWIFVNAGGMGSMCLLHSLSEYVLLFGTAIDTGGHSGRYWADISDTVITG	130	
Qy	118	-----GETVVHGPGEATAVEWGPNTMMVYGRGVIPSTLAFALADTVF	160	
Db	131	TFPROWKGGTYKSEVYFGDITLVHVAGENTSVMHSGGTMMVYGRGFIPSTMGFALADHIF	190	
Qy	161	STQDFLTLFVTLRSYARGRLRLTTYL	187	
Db	191	STQDFCTLFVTFRIYARCLLLETTYL	217	

RESULT 11

Q66IMI	PRELIMINARY;	PRT;	221 AA.
ID			
AC	Q66IMI;		
DT	25-OCT-2004 (TrEMBLrel. 28, Created)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)		
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)		
DE	Hypothetical protein.		
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodinae; Xenopus.		
OX	NCBI_TaxID=8364;		
OX	[1]		
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Whole body;		
RC	PubMed=12477932; DOI=10.1073/pnas.242603899;		
RC	Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Strausberg R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,		
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh P.,		
RA	Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,		
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,		
RA	Faney J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Whole body;		
RC	Klein S., Gerhard D.S.;		
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; EC081282; AAH81282.1; --		
DR	InterPro; IPR006716; ERG2_Sireceptlik.		
DR	Pfam; PF04622; ERG2_Sigmainr; 1.		
SW	Hypothetical protein.		
Q66IMI	SEQUENCE 221 AA; 24601 MW; 21E5CD2C3CD73F6F CRC64;		

Query Match	62.0%;	Score 629.5;	DB 2;	Length 221;
Best Local Similarity	56.6%;	Pred. No. 3.9e-49;		
Matches 120;	Conservative 32;	Mismatches 27;	Indels 33;	Gaps 2
Qy	9	WAWAAALLAVA--AVLTQVVWVLWLGTSQVFQREIEIAQLAROYAGLDHDLAFSLRIVELR	66	
Db	4	WRGLRAVLAVAGLAVAVQLLRGLWGSYSYFVNRREEIARLAKHEGLDYEVAFSKIITELR	63	
Qy	67	RLHPGHVLPDEELQWVFNAGGWMGACMLLHASLSEYVLLFGTALGSRGHS-----	117	
Db	64	KKHGPRILPDEDLQWVFNAGGWMGSCMLLHASLTYEVYLLFGTAVDTSGHSGRYWAEISD	123	
Qy	118	-----GETVHVGCEATAVWGPNMTWVVEYGRGVPISPLAAL	155	
Db	124	TILSGTTRQWKEGSKSEIIFPGDTIIVHEVGEATSVQWSAGTWMVEYGRGVPISPLGAL	183	
Qy	156	ADTVFSQDFLTLLFYTLRSYARGLRLELTYYL	187	
Db	184	ADTIFSTODELTLLFYTVKVGKALLLETSTHLL	215	

RESULT	12
Q7ZWG9	PRELIMINARY; PRT; 222 AA.
ID	Q7ZWG9
AC	O7ZMG9;
DT	01-JUN-2003 (TrEMBLrel. 24, Created)
DT	01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Similar to opioid receptor, sigma 1.
GN	ORFNames=29c:56378;
OS	GnBrachydanio rerio (zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Whole body;
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.
RA	Brownstein M.J., Ussdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.
RA	Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.
RA	Whitesley M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.
RT	"generation and initial analysis of more than 15,000 full-length hum
RT	and mouse cDNA sequences."
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Whole body;
RA	Strausberg R.,
RL	Submitted (MAR-2003) to the ENBL/GenBank/DBJ databases.
DR	ENBL; BC049416; AAH49416.1; -
DR	ZFIN; ZDB-GENE-040426-1006; rgic:56378.
DR	GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR	GO; GO:0002471; F:C-8 sterol isomerase activity; IEA.
DR	GO; GO:0004872; R:receptor activity; IEA.
DR	GO; GO:0006696; P:ergosterol biosynthesis; IEA.
DR	InterPro; IPR006716; ERG2_Slireceptlik.
DR	Pfam; PF04622; ERG2_SigmaIR; 1.

```

KW RECEPTOR.
SQ SEQUENCE 106 AA; 11992 MW; 8A4PDBFAFF6DAEE CRC64;

Query Match 53.5%; Score 544; DB 2; Length 106;
Best Local Similarity 98.1%; Pred. No. 1.1e-41;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQWAGRRWAWAALLAVAVLTQVWLWLGTSFVFORREEIAQLARQYAGLDHDLAFSR 60
Db 1 MQWAGRRWAWAALLAVAVLTQVWLWLGTSFVFORREEIAQLARQYAGLDHDLAFSR 60

QY 61 LIVELRRLHPGHVLPDEELQWVFNAGGWMGMCLLHASLSEVVL 105
Db 61 LIVELRRLHPGHVLPDEELQWVFNAGGWMGMCLLHASLSEALL 105

RESULT 14
Q9R1J7 PRELIMINARY; PRT; 106 AA.
AC Q9R1J7;
DT 01-MAY-2000 (T=EMBLrel. 13, Created)
DT 01-MAY-2000 (T=EMBLrel. 13, Last sequence update)

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_taxid=101116;
[1]
SEQUENCE FROM N.A.
RA Mei J., Pasternak G.W.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087827; AAD49439.1; -.
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR GO; GO:0000247; F:C-8 sterol isomerase activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006696; P:ergosterol biosynthesis; IEA.
DR InterPro; IPR006716; ERG2_Sireceptlik.
DR Pfam; PF04622; ERG2_SigmaIR; 1.
KW Receptor.
SQ SEQUENCE 106 AA; 12153 MW; 8BA4159B6A9E2A0F CRC64;

Query Match 50.0%; Score 508; DB 2; Length 106;
Best Local Similarity 89.5%; Pred. No. 2e-38;
Matches 94; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

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Db 1 MPWAVGRRWAWITLFTIVAVLIQAVWLGTGTSFVFORBEIAQLARQYAGLDHIAFSR 60

Qy 61 LIVELRLRHPGHVLPDBELQVFNAGGWMGAMCLLHASISEYVL 105
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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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OS Name=9G6.010;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetiales; Sordariales; Sordariaceae; Neurospora.
ON NCBI_Taxid=5141;
[1]
SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hobeisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 13:02:26 ; Search time 3089 Seconds
(without alignments)
9082.412 Million cell updates/sec

Title: US-09-823-069A-1
Perfect score: 579
Sequence: 1 atgcagtgggccgtggccg.....tctttggccaggacccttga 579

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_ba.*
2: gb_hlg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_ey.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	100.0	579	9 AF226604	Homo sapi
2	483	83.4	1598	9 BC007839	Homo sapi
3	483	83.4	1656	6 AX364934	Sequence
4	476	82.2	1641	9 HSU75283	Human sigma
5	476	82.2	1650	9 HSU79528	Human SR317
6	476	82.2	1655	6 CQ718427	Sequence
7	476	82.2	1679	9 BC004899	Homo sapi
8	476	82.2	1696	9 AK130502	Homo sapi
9	476	82.2	1700	6 BD076706	Human sig
10	472.8	81.7	672	9 CR457075	Homo sapi
11	438.2	75.7	579	10 AF226605	Mus muscu
12	375.2	64.8	1857	10 CFSIRECMR	C. porcellu
13	374.2	64.6	1070	10 AF087827	Rattus no
14	362.4	62.6	1117	10 AF067769	Rattus no
15	362.4	62.6	1621	10 BC061978	Rattus no
16	360.8	62.3	1590	10 AF004218	Rattus no
17	338.4	58.4	1567	10 AF030198	Mus muscu
18	338.4	58.4	1579	10 BC019930	Mus muscu
19	338.4	58.4	1595	10 BC002000	Mus muscu

20	338.4	58.4	1618	10 AF004927	Mus muscu
21	293.8	50.7	1501	9 AK098451	Homo sapi
22	235.6	40.7	34008	9 AL450283	Human DNA
23	227	39.2	1630	9 HSTIRG3	Homo sapi
24	218.2	37.7	1757	9 HSTIRG2	Homo sapi
25	203.4	35.1	1471	5 AJ719850	Gallus ga
26	188.8	32.6	1144	5 BC077894	Xenopus l
27	186.6	32.2	531	11 BV105885	MARC 8219
28	185.8	32.1	238811	2 AC098197	Rattus no
29	185.8	32.1	242324	2 AC110351	Rattus no
30	182.6	31.5	3954	9 AY007200	Homo sapi
31	182	31.4	6973	10 AF030199	Mus muscu
32	182	31.4	168268	10 AL807796	Mouse DNA
33	171	29.5	1202	5 BC081292	Xenopus t
34	169.4	29.3	1626	5 AY726668	Taricha g
35	157.6	27.2	1175	5 BC049416	Danio rer
36	136	23.5	158408	2 BX927402	Danio rer
37	127	21.9	202	6 AR269663	Sequence
38	65.4	11.3	645	6 AB6248	Sequence
39	65.4	11.3	645	6 AR155741	Genome DNA
40	65.4	11.3	645	6 E66266	Ermothec
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43	56.2	9.7	1296	6 BD179658	Highly th
44	54.2	9.4	85652	2 AC150118	Gallus ga
45	54.2	9.4	99981	2 AC150132	Gallus ga

ALIGNMENTS

RESULT 1	AF226604	Homo sapiens sigma 1 receptor beta variant mRNA, complete cds,	579 bp	mRNA	linear	PRI 18-APR-2000
LOCUS	AF226604	alternatively spliced.				
DEFINITION	AF226604					
ACCESSION	AF226604.1	GI:7582319				
VERSION						
KEYWORDS						
SOURCE		Homo sapiens (human)				
ORGANISM		Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE		1 (bases 1 to 579)				
AUTHORS		Wang,L.-M., Shelness,G.S., Childers,S.R., Mach,R.H. and Wheeler,K.T.				
TITLE		Sigma 1 beta receptor, an alternative splice variant of the sigma 1 receptor				
JOURNAL		Unpublished				
REFERENCE		2 (bases 1 to 579)				
AUTHORS		Wang,L.-M., Shelness,G.S., Childers,S.R., Mach,R.H. and Wheeler,K.T.				
TITLE		Direct Submission				
JOURNAL		Submitted (19-JAN-2000) Radiology, Wake Forest University School of Medicine, Medical Center Blvd., Winston-Salem, NC 27157, USA				
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      Best Local Similarity 84.8%; Pred. No. 1.9e-67;
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      QY 61 GTGCTGACCCAGGTGCTGTGGCTGTGGCTGGGTACGACAGAGTTCGTCTTCCAGCGCAA 120
      DB 61 GTGCTGATCCAGCGCGCTGTTGTGGCTGGGCACACAAAACITTCGTTCTCTAGAGAA 120
      QY 121 GAGATAGCGAGTTGGCGCGGACGATGCTGGCGTGGCTGACACAGAGCTGGCTCTCTCGT 180
      DB 121 GAAATAGCGAGCTTGTCTGACAGTATGCGGGGCTGGACCATGAGCTTGCCTTCTCTCG 180
      QY 181 CTGATCGTGAGCTGGCGCGCTGCACCCAGGCGACGCTGTGCCGACGAGGAGCTGCAG 240
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      QY 481 AGCACCCAGACTTCTCACCTTCTTATACCTTCTGCTCTTATGCTCGGGGCTCCGG 540
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      DEFINITION     Z66537
      ACCESSION      Z66537.1 GI:1403299
      VERSION        sigma1-receptor; sterol-isomerase.
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SOURCE
  ORGANISM      Cavia porcellus (domestic guinea pig)
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  Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
  REFERENCE
  1 (bases 1 to 1857)
  AUTHORS      Hanner,M., Moebius,F., Flandorfer,A., Knaus,H.G., Striessnig,J.,
  Kempner,E. and Glossmann,H.
  TITLE        Purification, molecular cloning, and expression of the mammalian
  signal-binding site
  JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 93 (15), 8072-8077 (1996)
  MEDLINE      96353947
  PUBMED      8755605
  REFERENCE
  2 (bases 1 to 1857)
  AUTHORS      Hanner,M.
  TITLE        Direct Submission
  JOURNAL      Submitted (26-OCT-1995) Hanner M., Universitaet Innsbruck,
  Biochemische Pharmakologie, Peter-Mayr-Str. 1, Innsbruck, Austria,
  A-6020
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        QY 61 GTGCTGACCCAGAGTCTGTGGCTGTGGCTAGCCAGAGCTTCGTTCCAGCGCGAA 120
        DB 438 GTTCTAACCAATTCGTGTGGCTCTGGCTGGGCACGACAGAACTTCGTTCTCCAGCGCGAA 497
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        QY 181 CTGATCGTGAGAGTGGCGCGCTGCACCCAGGCCACGCTGTGCCCGACGAGAGCTCGAG 240
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        QY 241 TGGGTGTTCTGTAATGCGGCTGCTGATGGCGCGCATGTGCCCTTCTGCACGCTCGCTG 300
        DB 618 TGGGTGTTCTGTAACGCGGCGCTGATGGCGCGCATGTGCCCTTCTGCATGCCCTCGCTG 677
        QY 301 TCCGAGTATGCTGCTCTTCCGACACCGCTTGGGCTTCCCGCGGCCACTCG----- 351
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        QY 352 ----- 351
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Db 798 ACCAAAAGTGAGGTCTTATCTACAGGGAGACAGTGGTGCACGGGCTTGGTGAAGCAACG 857
Qy 388 GCTGTGAGTGGGGCCAAACACATGGATGGTGGAGTACGGCCGGGGCTCATCCCATCC 447
Db 858 GCTGTGGAATGGGGACCAAAACACATGGATGGTGGAGTACGGCCGGGGTGTATCCCGTCT 917
Qy 448 ACCCTGGGCTTCGGGCTGGCCGACACTGTCTTCAGCACCCAGGACTTCTCTCACCCCTCTTC 507
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Qy 508 TATACCTTCGCTCCTATGCTCGGGGCTTCGGGCTTGAGCTCACCACTACTCTTTGGC 567
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Qy 568 CAGGACCCCTTGA 579
Db 1038 CAAGACCCCTTGA 1049

RESULT 13
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DEFINITION Rattus norvegicus sigma 1 receptor mRNA, alternatively spliced,
complete cds.
ACCESSION AF087827
VERSION AF087827.1 GI:57333129
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
REFERENCE 1 (bases 1 to 1070)
AUTHORS Mei, J. and Pasternak, G.W.
TITLE Molecular Cloning and Characterization of Rat Sigma 1 Receptor and
Its Splice Isoform
JOURNAL Unpublished
AUTHORS Mei, J. and Pasternak, G.W.
TITLE Direct Submission
JOURNAL Submitted (28-AUG-1998) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Ave., New York, NY 10021, USA
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Qy 375 TGGTACGGCAACAGCTGTGGAGTGGGGGCCAAAACACATGGATGGTGGAGTACGGCGGG 434
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Db 571 TGTATTCCGCTACCCCTGGCATTTGCACCTTAGTGACACTATTTTTCAGCAGCCAGACTT 630
Qy 495 CCTCACCTCTTCTATCTCTTCGCTCTGCTCGGGGCGCTTCGGGCTTGGAGTACACAC 554
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Qy 555 CTACCTCTTTGGCGGAGGACCCCTTGA 579
Db 691 CTACCTCTTTGGCGGAGGACCCCTGA 715

RESULT 14
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LOCUS Rattus norvegicus sigma 1 receptor mRNA, linear ROD 03-JUN-2004
DEFINITION Rattus norvegicus sigma 1 receptor mRNA, complete cds.
ACCESSION AF067769
VERSION AF067769.1 GI:6434854
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
REFERENCE 1 (bases 1 to 1117)
AUTHORS Mei, J. and Pasternak, G.W.
TITLE Molecular cloning and pharmacological characterization of the rat
sigma receptor
JOURNAL Biochem. Pharmacol. 62 (3), 349-355 (2001)
MEDLINE 21328659
PUBMED 11434908
REFERENCE 2 (bases 1 to 1117)
AUTHORS Mei, J. and Pasternak, G.W.
TITLE Direct Submission
JOURNAL Submitted (21-MAY-1998) Neurology, Memorial Sloan-Kettering Cancer
Center, 1275 York Avenue, New York, NY 10021, USA
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CDS

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 10:54:55 ; Search time 479 Seconds
(without alignments)

7155.595 Million cell updates/sec

Title: US-09-823-069A-1

Perfect score: 579

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: Geneseqn1990s:*
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- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	476	82.2	1655	12	ADQ87384 Human tum
5	476	82.2	1700	2	AAK39478 Human sig
6	473	81.7	696	6	AAH77235 Human sig
7	438.2	75.7	579	3	AAS15570 DNA encod
8	387	66.8	1535	3	AAF21650 Human bre
9	360.8	62.3	1590	10	ADB58553 Toxicity-
10	158.4	27.4	442	9	ACH50720 Human mam
11	127	21.9	202	10	ACA55628 Human sig
12	127	21.9	202	12	AD155424 Human pol
13	93	16.1	498	9	ACH45312 Human foe
14	65.4	11.3	645	2	ADR02215 A. gossyp
15	51.4	8.9	669	10	ADK65614 Yeast C8-
16	51.4	8.9	669	13	ADS47159 Bacterial
17	51.4	8.9	1508	2	AAT11777 S. cerevi
18	49.6	8.5	1052	13	Adt44395 Bacterial
19	49	8.5	633	6	ABA94360 Human FGF
20	49	8.5	636	6	ABV78180 Human FGF

21	49	8.5	636	6	AB235756 Human FGF
22	49	8.5	636	6	ABK86901 Human fib
23	49	8.5	636	6	ABX09999 Human FGF
24	49	8.5	636	6	ABL91721 Human pol
25	49	8.5	701	6	ABA94359 Human FGF
26	49	8.5	1330	4	AAS15701 Human fib
27	48.6	8.4	3018	8	AAL61203 Actinosyn
28	48.6	8.4	82746	8	AAL61224 Actinosyn
29	47.4	8.2	633	5	AAF62049 Human fib
30	47.4	8.2	633	6	ABN84523 Human fib
31	47.4	8.2	633	6	ABK13368 Human CDN
32	47.4	8.2	633	8	ACF57059 Human fib
33	47.4	8.2	633	10	ABQ83437 Human fib
34	47.4	8.2	633	12	AD391174 Human FGF
35	47.4	8.2	633	12	ADE39206 Human FGF
36	47.4	8.2	633	12	ADM57640 Human fib
37	47.4	8.2	636	3	AA75630 Nucleotid
38	47.4	8.2	636	5	AAS03277 Human CDN
39	47.4	8.2	636	6	AAD39242 Human FGF
40	47.4	8.2	636	8	ACF57077 Human FGF
41	47.4	8.2	636	12	ABK13369 Human DNA
42	47.4	8.2	814	6	ABK13369 Human DNA
43	47.4	8.2	814	8	ACF57060 Human fib
44	47.4	8.2	814	10	ABQ83442 Human fib
45	46.8	8.1	855	13	ADS49360 Bacterial

ALIGNMENTS

RESULT 1
AAS15569
ID AAS15569 standard; cDNA; 579 BP.
XX
AC AAS15569;
XX
DT 29-JAN-2002 (first entry)
XX
DE DNA encoding human sigma 1 receptor splice variant, sigma1beta.
XX
KW Human; sigma 1 receptor; sigma1beta; tumour imaging; cancer;
KW cell proliferation disorder; tumour; diagnostic; cytostatic; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..579
FT /*tag= a
FT /product= "Sigma 1 receptor splice variant sigma1beta"
XX
PN WO200174297-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US010650.
XX
PR 31-MAR-2000; 2000US-0193694P.
XX
PA (UYWA-) UNIV WAKE FOREST.
XX
PI Wheeler KT, Mach RH, Childers S, Shelness G, Wang L;
XX
DR WFI; 2001-662943/76.
DR P-PSDB; AAU09154.
XX
PT Novel isolated polynucleotide encoding sigma1beta receptor useful in
PT screening assay to identify ligands specific for the sigma1beta receptor
PT for tumor imaging, diagnostic and treatment methods.
XX
PS Claim 1; Fig 2; 56pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding sigma 1
CC receptor splice variant isolated from mouse adenocarcinoma cells and

CC human breast tumour cells. (I) or the encoded protein (II) is useful for
CC screening compounds useful in the imaging and treatment of proliferative
CC masses (i.e. tumours) and in the non-invasive diagnosis of cancer,
CC preferably in the diagnosis of proliferative cancer cells. (I), a cell
CC comprising (I), or (II) is useful in screening assays to identify ligands
CC specific for the sigma 1 receptor, and identification of the sigma 1
CC receptor permits the design of tumour imaging, diagnostic and treatment
CC methods. (I) is useful for preparing (II), which is useful as immunogen
CC for making antibodies. These antibodies are useful for a variety of
CC diagnostic and imaging purposes. Sigma 1 ligands obtained from screening
CC are useful as diagnostic compounds for imaging of, for example, tumour
CC cells, for determining the proliferative status of the tumour, and as
CC therapeutics for the treatment of cancer and other disorders of cell
CC proliferation. The present sequence represents the coding sequence of
CC human sigma 1 receptor splice variant, sigma1beta, as described in the
CC invention
XX
XX
SQ Sequence 579 BP; 76 A; 184 C; 199 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 579; DB 4; Length 579;
Best Local Similarity 100.0%; Pred. No. 8.8e-119;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGCAGTGGCGCGTGGCGCGGCTGGCGCGGCTGCTCTGGCTCTCGCAGCG 60
DB 1 ATGCAGTGGCGCGTGGCGCGGCTGGCGCGGCTGCTCTGGCTCTCGCAGCG 60
QY 61 GTGCTGACCCAGGTCTGCTGGCTCTGGCTGGGTAGCAGAGCTTCTCTTCCAGCGCAA 120
DB 61 GTGCTGACCCAGGTCTGCTGGCTCTGGCTGGGTAGCAGAGCTTCTCTTCCAGCGCAA 120
QY 121 GAGATAGCCAGTTGGCGCGGACGTACGCTGGGCTGGACACAGAGTGGCTCTCTCTGT 180
DB 121 GAGATAGCCAGTTGGCGCGGACGTACGCTGGGCTGGACACAGAGTGGCTCTCTCTGT 180
QY 181 CTGATCGTGGAGTGGCGCGGCTGACCCAGGCGCAGTCTGCTGCCAGGAGGCTGCGAG 240
DB 181 CTGATCGTGGAGTGGCGCGGCTGACCCAGGCGCAGTCTGCTGCCAGGAGGCTGCGAG 240
QY 241 TGGGTGTTCTGTAATCGCGGTGGCTGGATGGCGCCATGTCCTTTCACCGCTCGCTG 300
DB 241 TGGGTGTTCTGTAATCGCGGTGGCTGGATGGCGCCATGTCCTTTCACCGCTCGCTG 300
QY 301 TCGAGTATGTGCTCTTTCGACCGCTTGGGCTCCCGGGCCACTCGGGGGAGAGCG 360
DB 301 TCGAGTATGTGCTCTTTCGACCGCTTGGGCTCCCGGGCCACTCGGGGGAGAGCG 360
QY 361 GTAGTACACGGCGCTGGTGGAGCAACAGCTGTGGAGTGGGGGCCAAACACATGGATGGTG 420
DB 361 GTAGTACACGGCGCTGGTGGAGCAACAGCTGTGGAGTGGGGGCCAAACACATGGATGGTG 420
QY 421 GAGTACGGCGGGGGCTCATCCATCCACCTGGCCTTCGCGCTGGCGGACACTGTCTTC 480
DB 421 GAGTACGGCGGGGGCTCATCCATCCACCTGGCCTTCGCGCTGGCGGACACTGTCTTC 480
QY 481 AGCACCAGGACTTCTCTACCTCTTCTATCTTCTGCTCTCTGCTCTGCTGGGCGCTCGG 540
DB 481 AGCACCAGGACTTCTCTACCTCTTCTATCTTCTGCTCTCTGCTCTGCTGGGCGCTCGG 540
QY 541 CTTGAGCTCACCACCTTACCTCTTTGGCCAGGACCTTTGA 579
DB 541 CTTGAGCTCACCACCTTACCTCTTTGGCCAGGACCTTTGA 579

RESULT 2
ABL39775
ID ABL39775 standard; cDNA; 1656 BP.

XX ABL39775;

XX 10-MAY-2002 (first entry)

DE Human NS cDNA sequence SEQ ID NO:85.

XX Human; cytostatic; osteopathic; gynaecological; neuromuscular; anti-HIV;
KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; dermatological;
KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
KW anorectic; muscular; antinfertility; cardiovascular; anticoagulant;
KW antifibrinolytic; hypotension; antiaesthetic; immunomodulator; cardiac;
KW anticonvulsant; antidiabetic; tranquiliser; antipressant; neuroleptic;
KW gastrointestinal; virucide; antitumor; cancer; osteoporosis; dysomnia;
KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dysomnia;
KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
KW infertility; cardiovascular disease; coagulation disease; hypertension;
KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
KW gastric ulcer; Alzheimer's disease; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200206315-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-IL000653.
XX
PR 18-JUL-2000; 2000IL-00137345.
PR 15-DEC-2000; 2000IL-00140354.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Mintz L, Freilich S, Bernstein J;
XX
DR WPI; 2002-155037/20.
DR P-FSDB; ABB06121.
XX
PT One hundred and twenty eight novel nucleic acid sequences, useful for
PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
XX
PS Claim 1; Page 126; 290pp; English.

XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
CC anorectic, muscular, anti-HIV, antinfertility, cardiovascular, cardiac,
CC anticoagulant, antifibrinolytic, hypotension, antidiabetic, tranquiliser, antitumor,
CC immunomodulator, anticonvulsant, antidiabetic, antipressant, neuroleptic,
CC antipressant, gastrointestinal, antitumor, antitumor, antitumor, antitumor,
CC gene therapy and antitumor therapy. Nucleic acids, expression vectors and
CC antibodies from the present invention can be used for treating and
CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
CC diseases, dysomnia, multiple sclerosis, rheumatoid arthritis, psoriasis,
CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
CC depression, epilepsy, angina, neurodegeneration, diabetes, anxiety,
CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
CC Alzheimer's disease and as a contraceptive

XX
SQ Sequence 1656 BP; 342 A; 508 C; 458 G; 346 T; 0 U; 2 Other;

Query Match 83.4%; Score 483; DB 6; Length 1656;
Best Local Similarity 88.6%; Pred. No. 1.9e-97;
Matches 554; Conservative 0; Mismatches 25; Indels 46; Gaps 1;

QY 1 ATGCAGTGGCGCGTGGCGCGGCTGGCGCGGCTGCTCTGGCTCTCGCAGCG 60
DB 118 ATGCAGTGGCGCGTGGCGCGGCTGGCGCGGCTGCTCTGGCTCTCGCAGCG 177
QY 61 GTGCTGACCCAGGTCTGCTGGCTCTGGCTGGGTAGCAGAGCTTCTCTTCCAGCGCAA 120
|||||

Db	615	ACCGTGGCTTCGGCGTGGCGGACACTGCTTTACGACACCGAGGACTTCCTCACCCCTCTTC	674
Qy	508	TATACTCTTCGCTCTCTATGCTCGGGGCTTCGGGTGAGCTCACCACTTACTCTCTTTGGC	567
Db	675	TATACTCTTCGCTCTCTATGCTCGGGGCTTCGGGTGAGCTCACCACTTACTCTCTTTGGC	734
Qy	568	CAGGACCCCTTGA	579
Db	735	CAGGACCCCTTGA	746

RESULT 4	
ADQ87384	
ID	ADQ87384 standard; cDNA; 1655 BP.
XX	
AC	ADQ87384;
XX	
DT	07-OCT-2004 (first entry)
XX	
DE	Human tumour-associated antigenic target (TAT) cDNA sequence #4261.
XX	
KW	human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
KW	cancer; cell proliferative disorder; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO2004060270-A2.
XX	
PD	22-JUL-2004.
XX	
PF	15-OCT-2003; 2003WO-US029126.
XX	
PR	18-OCT-2002; 2002US-0418988P.
XX	
PA	(GETH) GENENTECH INC.
PA	(WUTD/) WU T D.
PA	(ZHOU/) ZHOU Y.
XX	
PI	Wu TD, Zhou Y;
XX	
DR	WPI; 2004-534300/51.
XX	
PT	New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT	preventing or treating cell proliferative disorders such as cancer.
XX	
PS	Claim 1: SEQ ID NO 4261; 5504bp; English.

presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytosratic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

RESULT 5
AAx29478
ID AAX29478 standard; DNA; 1700 BP.
XX
AC AAX29478;

Db 488 CTTACGACCCAGGACTTCTCACCCCTCTTCTATACCTCTTGCTCTCTATGCTCGGGCCT 547

Qy 537 CGGGCTTGAGCTCACACCTACCTCTTTGGCCAGACCCCTTGA 579

Db 548 CGGGCTTGAGCTCACACCTACCTCTTTGGCCAGACCCCTTGA 590

RESULT 9
ADB58553
ID ADB58553 standard; DNA: 1590 BP.

AC ADB58553;

DT 04-DEC-2003 (first entry)

XX DE Toxicity-related gene. SEO ID 3579.

KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
 KW drug screening; toxicity assay; ds.

Unidentified.

PN WO2003064624-A2

XX
PD
07-AUG-2003XX
PE
31 -JAN-2003- 2003WO-IJS003194-

31-JAN-2003 2003US-00060087

PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P

PR 30-DEC-2002; 2002US-0436643P.
vv

PA (GENE-) GENE LOGIC INC.

PI Mendrick D, Porter M,

DR WPI; 2003-689530/65.

PT Predicting a toxic e

PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.

PS Claim 1; SEQ ID NO 3579; 1156pp; English.

The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at least one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published/pct_sequences.

Sequence 1590 BP; 347 A; 435 C; 447 G; 361 T; 0 U; 0 Other;

Query Match	62.3%	Score 360.8;	DB 10;	Length 1590;
Best Local Similarity	75.4%	Pred. No. 2.1e-70;		
Matches 507; Conservative	0;	Mismatches 72;	Indels 93;	Gaps 1;

Qy

1 ATGCAGTGGCCGTGGGCCCGGCGGTGGCGCGCTCTCTGGCTTCGCAGCG 60
|||||

Dδ

39 ATGCCGTGGGCTGTGGGCGCGGTGGGCATGGATCACCCCTGTTTCTGACATTATTGGCG 98
|||||

Qy	61	GTGCTGACGAGTTCGTGCTGGCTGGGTACGACAGCTTCGTCTTCCAGCGCGNA	120
Db	99	GTGCTGATCCAGGCGGTCTGGCTGGGTGAGTCTCAGAGCTTCGTCTTCCAGAGAGAA	158
Qy	121	GAGATAGCGAGTTGGCGCGGACGTACGCTGGGCTGGACACGAGCTGGCCCTTCTCTCGT	180
Db	159	GAGATAGCTCAGCTTGTCTGACAGTACGACGGCTGGACCATGAGCTGGCCCTTCTCTCGG	218
Qy	181	CTGATCTGGAGCTCGCGCGGCTGCACCCAGGCCACGTTGCTGCCGACGAGAGCTGCAG	240
Db	219	CTGATCTGGAGCTCGCGAGGCTGCACCCAGGCCACGCTGCTGCCGATGAGAGCTGCAG	278
Qy	241	TGGGTGTTCTGAATGCGGGTGGCTGATGGGCGGCATGTGCTTCTGCACGCCCTCGCTG	300
Db	279	TGGGTGTTTGTGAACGCGGGCGGCTGGATGGGCGCCATGTGTCTTTTGCACGCCCTCGCTG	338
Qy	301	TCCGAGTATGTGCTGCTCTTCGGGCACCGCCCTTGGGCTCCCGGGCACCTCG	351
Db	339	TCTGAGTACGTGCTGCTCTTCGGGCACCGCCCTGGGCTCCCATGGCCATTGGGGACGATAC	398
Qy	352	-----	351
Db	399	TGGGCTGAGATTTCAGATACCATCATCTCTGGCACTTTCCACCAGTGGAGAGGGGCACC	458
Qy	352	-----GGGGAGACGCTAGTACACGGGCTGGTGGAGGCAACA	387
Db	459	ACAAAAAGTGAGGTCTATTACCCAGGAGAGACGGTTGTCCATGGACCTGGAGAGGCAACA	518
Qy	388	GCTGTGAGTGGGGGCGGCAACACATGGATGGTGGAGTACGGCCGGGGCGGTATCCCATCC	447
Db	519	GATGTGAGTGGGACCAACACGTTGATGGTGGAGTATGGCCGGGCTTTATTCCGCTCT	578
Qy	448	ACCTGGCCTTGGCGCTGGCGGACACTGTCTTCCAGCACCCAGGACTTCCTCAACCTCTTC	507
Db	579	ACCTGGCAATTTGCACCTTAGTGACACTATTTTCAGCACCCAGGACTTCCTCAACCTCTTC	638
Qy	508	TATACCTTTCGCTCCTATGCTCGGGGCTCCGGCTTGAGCTCACCACTACCTCTTTGGC	567
Db	639	TATACCTTTCGCGCTATGCCCGGGGCTCCGGCTTGAGCTCACCACTACCTCTTTGGC	698
Qy	568	CAGGACCCCTTGA 579	
Db	699	CAAGACCCCTGA 710	
RESULT 10			
ACH50720			
ID ACH50720 standard; cDNA; 442 BP.			
AC	ACH50720;		
AC			
XX	13-OCT-2003 (first entry)		
XX	Human mammary gland cDNA #125.		
XX	Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;		
XX	genome mapping; biodiversity; genetic disorder.		
XX	Homo sapiens.		
XX	US2003073623-A1.		
PN	17-APR-2003.		
XX	30-JUL-2001; 2001US-00918995.		
XX	30-JUL-2001; 2001US-00918995.		
XX	(DRMA/) DRMANAC R T.		
PA	(LABA/) LABAT I.		
PA	(STAC/) STACHE-CRAIN B.		
PA	(DICK/) DICKSON M C.		


```
DT 23-SEP-2004 (first entry)
XX
XX A. gossypii genomic DNA PAG1566RP.
XX
XX Filamentous funghi; ds; forensic identification; gene characterisation;
XX intergenomic comparison; chromosome mapping.
XX
XX Eremothecium gossypii.
XX
XX US6239264-B1.
XX
XX 29-MAY-2001.
XX
XX 24-DEC-1997; 97US-00998416.
XX
XX 31-DEC-1996; 97CH-00000016.
XX
XX (SYNG-) SYNGENTA PARTICIPATIONS AG.
XX
XX Philippe P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;
XX Knechtle P, Reibschung C;
XX
XX WPI; 1998-388120/33.
XX
XX New gene for adenylate cyclase from Ashbya gossypii - useful for
XX generating recombinant microorganisms with alteration in gene of cAMP-
XX dependent signalling pathway for increasing production of fine chemicals.
XX
XX Example 3; SEQ ID NO 907; 632pp; English.
XX
XX The invention relates to isolated DNA molecules comprising isolated
XX genomic DNA sequences from the filamentous funghi Ashbya gossypii, the
XX sequences comprising ADR01309, ADR01366, ADR01367, ADR01386, ADR01428,
XX ADR01466, ADR01629, ADR01637, ADR02057, ADR02345 and ADR02369, chosen
XX from 1047 disclosed genomic sequences. Also included is a cloning vector
XX comprising a nucleotide sequence chosen from the above sequences. The
XX novel Ashbya gossypii genomic sequences are useful for forensic
XX identification, gene characterisation, for studying gene organisation by
XX intergenomic comparison (with Saccharomyces cerevisiae), identifying
XX biosynthetic genes for selectable markers, to isolate
XX promoters/terminators/centromeres, chromosome mapping, and in identifying
XX sequences unique to Ashbya gossypii for species identification. The
XX present sequence is an A. gossypii novel genomic sequence of the
XX invention.
XX
XX Sequence 645 BP; 123 A; 196 C; 215 G; 111 T; 0 U; 0 Other;
XX
XX Query Match 11.3%; Score 65.4; DB 2; Length 645;
XX Best Local Similarity 68.7%; Pred. No. 5e-05;
XX Matches 90; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
XX
XX 227 ACGAGGAGTCAGTGGGTGTCGTGAATCGGGTGGCTGGATGGGGCCCATGTGCCTTC 286
XX 106 ACCTGGAGGACGAGTGGGTGTCACACACGGGGCGGGCTATGGGGCAGATGCTGATTC 165
XX 287 TGCACGCTCGTCTCCAGTATGTGCTCTTCGGCACCGCTTGGGCTCCCGGGCC 346
XX 166 TGCACGCGTCTGTGAGCGAGTACCTGATCTCTGTTCGGCAGCGCGCTGGGACGAGGGCC 225
XX
XX 347 ACTCGGGGGAG 357
XX 226 ACACGGGGCGTG 236
XX
XX RESULT 15
XX ADR65614
XX ID ADR65614 standard; DNA; 669 BP.
XX
XX ADR65614;
XX
XX 06-MAY-2004 (first entry)
XX
XX Yeast C8-isomerase gene.
```

```
XX ds; gene; yeast; delta8-delta7-isomerase; enzyme; 7-dehydrocholesterol;
XX vitamin D3; skin cream; terpene; steroid hormone synthesis; C8-isomerase.
XX
XX Saccharomyces cerevisiae.
XX
XX Key Location/Qualifiers
XX CDS 1..669
XX /tag= a
XX /product= "C8-isomerase"
XX
XX DE10203352-A1.
XX
XX 31-JUL-2003.
XX
XX 29-JAN-2002; 2002DE-01003352.
XX
XX 29-JAN-2002; 2002DE-01003352.
XX
XX (BADI ) BASF AG.
XX
XX Lang C, Veen M;
XX
XX WPI; 2003-732841/70.
XX P-PSDB; ADK65615.
XX
XX Preparation of 7-dehydrocholesterol, useful as an intermediate for
XX vitamin D3, and its intermediates or products, comprises growth of
XX PT organisms with increased activity of specific enzymes.
XX
XX Claim 15; Page 41-42; 120pp; German.
XX
XX The present invention relates to a method for the preparation of 7-
XX dehydrocholesterol, and/or its biosynthetic intermediates and/or
XX secondary products, which comprises culturing organisms that have,
XX relative to the wild type, increased activity of at least one of delta8-
XX delta7-isomerase, delta5-desaturase and/or delta24-reductase. 7-
XX dehydrocholesterol is an intermediate for Vitamin D3, and its
XX intermediates/secondary products (e.g. zymosterol, lanosterol, squalene,
XX farnesol, geraniol, cholesta-trienol or tetraenol), and useful for
XX synthesis of terpenes, in dermatology and cosmetics, in synthesis of
XX saponins and steroid hormones, and as emulsifiers in skin creams. The
XX present sequence is the S. cerevisiae C8-isomerase gene as used in the
XX method of the invention.
XX
XX Sequence 669 BP; 184 A; 151 C; 143 G; 191 T; 0 U; 0 Other;
XX
XX Query Match 8.9%; Score 51.4; DB 10; Length 669;
XX Best Local Similarity 65.0%; Pred. No. 0.064;
XX Matches 76; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
XX
XX 239 AGTGGGTGTTGCGATGCGGTGGCTGGATGGGGCCCATGTGCTTCTGCACGCCCTCGC 298
XX 245 AATGGGTCTTCAACAATGCTGGTGGTGGCGATGGGCCAAATGATCATCTTACAGCTTCCG 304
XX 299 TGTCCGAGTATGCTGCTCTTCGGCACCGCTTGGGCTCCCGGGGCACTTCGGGGG 355
XX 305 TATCCGAGTACTTAATTCCTGGAACCGCTGTTGGTACTGAAGGCAACACAGGTG 361
XX
XX Search completed: October 30, 2005, 16:08:09
XX Job time : 487 secs
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000

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Maximum Match 100%
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	476	82.2	1700	2	US-08-928-612-2
2	127	21.9	202	4	US-09-016-434-226
3	65.4	11.3	645	3	US-08-998-416-907
4	51.4	8.9	689	4	US-09-614-221A-181
5	51.4	8.9	1508	1	US-08-240-496A-1
6	51.2	8.8	2700	4	US-09-902-540-7680
7	51.2	8.8	6351	4	US-09-902-540-757
8	50.4	8.7	4263	4	US-09-902-540-4659
9	50.4	8.7	29384	4	US-09-902-540-1229
10	49.6	8.6	1404	4	US-09-902-540-6859
11	49.6	8.6	3875	4	US-09-902-540-579
12	49	8.5	1016	4	US-09-949-016-2934
13	48.8	8.4	2556	4	US-09-902-540-4939
14	48.8	8.4	30780	4	US-09-902-540-1243
15	48.6	8.4	13335	4	US-09-949-016-14676
16	47.6	8.2	6645	4	US-09-902-540-8819
17	47.6	8.2	10210	4	US-09-902-540-938
18	47.4	8.2	636	4	US-09-692-945-3
19	46.8	8.1	2235	1	US-08-418-782-1
20	46.8	8.1	2235	2	US-08-228-662-1
21	46.8	8.1	2235	1	US-08-852-219-1
22	46.8	8.1	2331	1	US-08-418-782-20
23	46.8	8.1	2331	2	US-08-852-219-20
24	46.8	8.1	4403765	3	US-09-103-840A-2
25	46.8	8.1	4411529	3	US-09-103-840A-1
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27	46	7.9	1458	4	US-09-252-991A-16310

28	46	7.9	1599	4	US-09-252-991A-16536
29	45	7.8	9132	4	US-09-949-016-13070
30	44.6	7.7	77536	4	US-09-410-551B-1
31	44.6	7.7	77536	4	US-09-940-316B-1
32	44.4	7.7	34094	4	US-09-292-034-1
C 33	44	7.6	4506	4	US-08-178-257-1
C 34	44	7.6	6977	4	US-08-178-257-8
35	43.8	7.6	2214	3	US-08-864-038A-1
36	43.8	7.6	3331	3	US-08-864-038A-2
37	43.8	7.6	3331	3	US-08-864-038A-4
38	43.8	7.6	41106	4	US-09-949-016-15796
39	43.6	7.5	1410	4	US-09-902-540-3735
C 40	43.6	7.5	19112	4	US-09-902-540-1181
C 41	43.2	7.5	696	4	US-09-252-991A-647
42	43.2	7.5	1371	4	US-09-252-991A-764
43	43.2	7.5	1392	4	US-09-252-991A-704
44	43.2	7.5	4826	4	US-09-772-304A-1
45	43.2	7.5	10424	4	US-09-902-540-1015

ALIGNMENTS

RESULT 1
US-08-928-612-2
; Sequence 2, Application US/08928612
; Patent No. 5863766
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN SIGMA RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,612
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0383 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1700 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTAT04
; CLONE: 1542751
US-08-928-612-2
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Best Local Similarity 86.2%; Pred. No. 4.8e-109;


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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 907:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1566RP
;
US-08-998-416-907

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Best Local Similarity 68.7%; Pred. No. 5.5e-07;
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DB 106 ACCTGGAGGACGAGTGGGTGTTCAACAACGCGGGCGCGTATGGGGCAGATGCTGATTC 165

QY 287 TGCACGCTCGCTGCGAGTATGCTGCTCTTCGGCACCGCTTGGGCTCCCGGGCC 346
DB 166 TGCACGCGTGTGAGCGAGTACTGATTCCTGTTGGCACGCGCGCTGGGACGAGGGCC 225

QY 347 ACTCGGGGGGAG 357
DB 226 ACACGGGCGTG 236

RESULT 4
US-09-614-221A-181
; Sequence 181, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 181
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
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US-09-614-221A-181

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RESULT 5
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; Sequence 1, Application US/08240496A
; Patent No. 5480805
; GENERAL INFORMATION:
; APPLICANT: Wolf, Fred R.
; APPLICANT: Cuellar, Richard E.
; TITLE OF INVENTION: Composition for Modulating Sterols in
; Yeast
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesser
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,496A
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,764
; FILING DATE: 12-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesser, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 31,456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1508 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 379..1047
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US-08-240-496A-1

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Best Local Similarity 65.0%; Pred. No. 0.0021;
Matches 76; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 239 AGTGGGTGTTTCGTAATGCGGGTGGCTGGATGGCGCATGTGCTTCTGCACGCTTCG 298
DB 623 AATGGGTCTTCAACAATGCTGGTGGTGGATGGCCAAATGATCATCTACACGCTTCG 682

QY 299 TGTCCGAGTATGTGCTCTCTTCGGCACCGCTTGGGCTCCCGGGCCACTCGGGGG 355
DB 683 TATCCGAGTACTTAATTCTATTCGGAACCGCTGTGTGCTACTGAAGGGCACACAGGTG 739

RESULT 6
US-09-902-540-7680
; Sequence 7680, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
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GenCore version 5.1.1.6
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- 22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq*
- 23: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 24: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq2*
- 25: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*
- 26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	328	56.6	1569	22	US-10-764-420-2180

6	208.2	36.0	684	19	US-10-240-425-1015	Sequence 1015, Ap
7	158.4	27.4	442	10	US-09-918-995-37932	Sequence 37932, A
8	127	21.9	202	18	US-10-305-720-226	Sequence 226, App
9	93	16.1	498	10	US-09-918-995-32524	Sequence 32524, A
10	51.4	8.9	669	18	US-10-369-493-25589	Sequence 25589, A
11	51.4	8.9	669	20	US-10-793-639-181	Sequence 181, App
12	49.6	8.6	680	19	US-10-425-114-12614	Sequence 12614, A
13	49.6	8.6	1052	18	US-10-369-493-42833	Sequence 42833, A
14	49.6	8.6	1602	21	US-10-425-115-124288	Sequence 124288,
15	49	8.5	636	20	US-10-384-339C-64	Sequence 64, Appl
16	49	8.5	1330	9	US-09-805-805-1	Sequence 1, Appli
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18	48.8	8.4	1632	19	US-10-425-114-24893	Sequence 24893, A
19	48.8	8.4	1636	19	US-10-425-114-2037	Sequence 2037, Ap
20	48.8	8.4	1693	21	US-10-425-115-78945	Sequence 78945, A
21	47.4	8.2	633	9	US-09-817-814-1	Sequence 1, Appli
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24	47.4	8.2	633	17	US-10-174-394-47	Sequence 47, Appl
25	47.4	8.2	633	17	US-10-174-394-49	Sequence 49, Appl
26	47.4	8.2	633	17	US-10-174-394-51	Sequence 51, Appl
27	47.4	8.2	633	17	US-10-174-394-53	Sequence 53, Appl
28	47.4	8.2	633	18	US-10-321-962-1	Sequence 1, Appli
29	47.4	8.2	633	21	US-10-435-087-3	Sequence 3, Appli
30	47.4	8.2	633	21	US-10-435-087-35	Sequence 35, Appl
31	47.4	8.2	633	22	US-10-948-588-1	Sequence 1, Appli
32	47.4	8.2	633	24	US-10-980-764-1	Sequence 1, Appli
33	47.4	8.2	633	24	US-10-980-764-21	Sequence 21, Appl
34	47.4	8.2	633	24	US-10-980-659-1	Sequence 1, Appli
35	47.4	8.2	633	24	US-10-980-659-21	Sequence 21, Appl
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38	47.4	8.2	633	26	US-11-027-948-1	Sequence 1, Appli
39	47.4	8.2	636	14	US-10-005-646-1	Sequence 1, Appli
40	47.4	8.2	636	14	US-10-090-983-4	Sequence 4, Appli
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43	47.4	8.2	636	24	US-10-980-764-5	Sequence 5, Appli
44	47.4	8.2	636	24	US-10-980-659-5	Sequence 5, Appli
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ALIGNMENTS

RESULT 1
US-09-823-069-1
; Sequence 1, Application US/09823069
; Patent No. US20020061847A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Kenneth
; APPLICANT: Mach, Robert
; APPLICANT: Childers, Steven
; APPLICANT: Shelness, Gregory
; APPLICANT: Wang, Li-Ming
; TITLE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE VARIANT
; TITLE OF INVENTION: SIGMA-1 RECEPTOR
; FILE REFERENCE: 9151.6
; CURRENT APPLICATION NUMBER: US/09/823,069
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,694
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-823-069-1

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RESULT 6
 S-10-240-425-1015
 Sequence 1015, Application US/10240425
 Publication No. US20040033502A1
 GENERAL INFORMATION:
 APPLICANT: Williams, Amanda
 APPLICANT: Boland, Joseph F.
 APPLICANT: Lord, Reginald V.
 APPLICANT: Alvarez, Chris
 APPLICANT: Wetzel, Jon C.
 APPLICANT: Scherif, Uwe
 APPLICANT: Vockley, Joseph G.
 TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
 FILE REFERENCE: 44921-5026
 CURRENT APPLICATION NUMBER: US/10/240,425
 CURRENT FILING DATE: 2002-09-30
 PRIOR APPLICATION NUMBER: PCT/US01/09847
 PRIOR FILING DATE: 2001-03-28
 PRIOR APPLICATION NUMBER: US 60/193,446

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Post-processing: Minimum Match 0%
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SUMMARIES

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10	476	82.2	884	1	AL543500 AL543500
11	476	82.2	894	1	AL532097 AL532097
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28	476	82.2	1592	3	CR604448 full-leng
29	476	82.2	1601	3	CR596218 full-leng
30	476	82.2	1606	3	CR609235 full-leng
31	476	82.2	1618	3	CR608948 full-leng
32	476	82.2	1619	3	CR625524 full-leng
33	476	82.2	1627	3	CR590434 full-leng
34	476	82.2	1627	3	CR602297 full-leng
35	476	82.2	1629	3	CR595153 full-leng
36	476	82.2	1631	3	CR611273 full-leng
37	476	82.2	1640	3	CR619527 full-leng
38	476	82.2	1644	3	CR603042 full-leng
39	476	82.2	1646	3	CR592762 full-leng
40	476	82.2	1654	3	CR611989 full-leng
41	476	82.2	1658	3	CR598930 full-leng
42	476	82.2	1659	3	CR593849 full-leng
43	476	82.2	1671	3	CR592515 full-leng
44	475.6	82.1	1093	1	AL520391 AL520391
45	474.4	81.9	916	1	AL531582 AL531582

ALIGNMENTS

RESULT 1
BI553398
LOCUS 603193344F1 NTH_MGC_95 Homo sapiens CDNA clone IMAGE:5264674 5',
DEFINITION mRNA sequence.
ACCESSION BI553398
VERSION BI553398.1 GI:154440710
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 852)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LHAM11667 row: g column: 11
High quality sequence stop: 824.

FEATURES
source

1. 852
Location/Qualifiers
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/clone="IMAGE:5264674"
/tissue_type="hippocampus"
/lab_host="DH10B"
/clone_l1b="NIH_MGC_95"
/notes="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."


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QY 181 CTGATCGTGGAGCTCGCGCGCTGCACCCAGGCCACGTGCTGCCGACGAGGAGCTGCAG 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
262 CTGATCGTGGAGCTCGCGCGCTGCACCCAGGCCACGTGCTGCCGACGAGGAGCTGCAG 321
QY 241 TGGGTGTTTCGTGAATCGCGGTGGCTGGATGGCGGCCATGTGCTTCTTCGACGCTCGCTG 300
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322 TGGGTGTTTCGTGAATCGCGGTGGCTGGATGGCGGCCATGTGCTTCTTCGACGCTCGCTG 381
QY 301 TCCGATGATGCTGCTCT- 319
Db |||||||||||||||||||
382 TCCGAGCGGCTACTCGGCTGAGATCTCGGATACCATCATCTCTGCGACCTTCCACAGTG 441
QY 320 -----TCGCGACCGCTTGGGCTCCGCGGCCACTCGCGGGAGAGCGGTAGTACAGGGCC 374
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
442 GAGAGAGGCGACACCAAAAGTGAAGTCTTACCCAGGGGAGAGCGGTAGTACAGGGCC 501
QY 375 TGGTGAGGCAACAGCTGTGGAGTGGGGGCGCAACACATGATGATGGTGGAGTACGGCGGGG 434
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QY 435 CGTCAATCCCATCCACCTCGGCTTCCGCTGGCGGACACATGCTTTCAGCACCCAGGACTT 494
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
562 CGTCAATCCCATCCACCTCGGCTTCCGCTGGCGGACACATGCTTTCAGCACCCAGGACTT 621
QY 495 CCTCACCTCTTCTATCTTCTGCTTCTGCTTCTGCTGCGGGCCTCCGGCTTGAGCTCACCAC 554
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 555 CTACCTCTTTGGCGGAGCCCTTTGA 579
Db |||||||||||||||||||
682 CTACCTCTTTGGCGGAGCCCTTTGA 706
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RESULT 5
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LOCUS BX463121 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM007Y109 5-PRIME, mRNA sequence.
ACCESSION BX463121
VERSION BX463121.2 GI:47064026
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 890)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31027522.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5104.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DM007Y109&loc=5104.r.
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/db_xref="taxon:9606"
/clone="CS0DM007Y109"
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/dev_stage="fetal"
/clone_lib="Homo sapiens FETAL LIVER"
/note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
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enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

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Best Local Similarity 88.5%; Pred. No. 6e-100;
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69 ATGCGCTGGCGCGTGGCGCGCGTGGCGCGCGCTGCGCTGCTGCTGCTGCTGTCGAGCG 128
QY 61 GTGCTGACCCAGGTCGTCTGGCTGCTGGCTGGGTAGCAGAGCTTCTTCCAGCGCGAA 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
129 GTGCTGACCCAGGTCGTCTGGCTGCTGGCTGGGTAGCAGAGCTTCTTCCAGCGCGAA 188
QY 121 GAGATAGCGCAGTGGCGCGCGCAGTACGCTGGGCTGGACACGAGCTGGCTTCTCTGT 180
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189 GAGATAGCGCAGTGGCGCGCGCAGTACGCTGGGCTGGACACGAGCTGGCTTCTCTGT 248
QY 181 CTGATCGTGGAGCTGGCGCGCGCTGCACCCAGGCGACGCTGCTGCCGACGAGAGCTGCAG 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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QY 241 TGGGTGTTTCGTGAATGCGGGTGGCTGGATGGCGCCCATGTGCTTCTGCAGCCCTCGCTG 300
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309 TGGGTGTTTCGTGAATGCGGGTGGCTGGATGGCGCCCATGTGCTTCTGCAGCCCTCGCTG 368
QY 301 TCCGAGTATGCTGCTCT- 319
Db |||||||||||||||||||
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429 GAGAGAGGCGCACCAAAAGTGAGGCTCTTCTACCCAGGGGAGACGCTAGTACACGGGCC 488
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Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
609 CCTCACCTCTTCTATCTTCTGCTTCTGCTTCTGCTGCGGGCCTCCGGCTTGAGCTCACCAC 668
QY 555 CTACCTCTTTGGCGGAGCCCTTTGA 579
Db |||||||||||||||||||
669 CTACCTCTTTGGCGGAGCCCTTTGA 693
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RESULT 6

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LOCUS BX324967 900 bp mRNA linear EST 27-FEB-2001
DEFINITION 602423618F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:4561493 5',
mRNA sequence.
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ACCESSION BG324967
VERSION BG324967.1 GI:13131508
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 900)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP

D	b	585	GCTGTGGAGTGGGGGCCAAACATGATGTTGAAGTAGCGCCGGGGCGTCA	TCCATCC	644
Q	y	448	ACCTTGCCCTTCGGCGCTGGCCGACA	CACTGTGTTTCAGCACCCAGGACTTCCTCACCCTCTTC	507
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Q	y	508	TATACTCTTCGCTCCTAAGCTCGGGGCT	CCGGCTTGAGCTCAACCACTTCTTTGGC	567
D	b	705	TATACTCTTCGCTCCTAAGCTCGGGGCT	CCGGCTTGAGCTCAACCACTTCTTTGGC	764
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LOCUS AL532097 Homo sapiens FETAL LIVER Homo sapiens cDNA clone					
DEFINITION CSODM004YL04 5-PRIME, mRNA sequence.					
ACCESSION AL532097					
VERSION AL532097.3 GI:45707026					
KEYWORDS EST.					
SOURCE Homo sapiens (human)					
ORGANISM Homo sapiens					
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
1 (bases 1 to 894)					
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.					
Full-length cDNA libraries and normalization					
Unpublished (2001)					
On Feb 13, 2001 this sequence version replaced gi:31069929.					
COMMENT					
Contact: Genoscope					
Genoscope - Centre National de Sequencage					
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE					
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr					
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime					
end enriched, double-strand cDNA was digested with Not I and cloned					
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library					
was not normalized. Library was constructed by Life Technologies, a					
division of Invitrogen.					
This sequence belongs to sequence cluster 5104.r					
For more information about this cluster, see					
http://www.genoscope.cns.fr/cdna?s=CSODM004DF02QP1&c=5104.r.					
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/clone="CSODM004YL04"					
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was primed with a NotI-oligo(dT) primer. Five prime end					
enriched, double-strand cDNA was digested with Not I and					
cloned into the Not I and EcoRV sites of the pCMVSPORT 6					
vector. Library was not normalized."					
ORIGIN					
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Best Local Similarity 86.2%; Pred. No.1e-98;					
Matches 579; Conservative 0; Mismatches 0; Indels 93; Gaps 1;					
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Q	y	61	GTGCTGACCCAGTTCGTTGCTCTGCTGGTGGTACGACAGCTTCGTTCCAGCGCGAA	120	
D	b	137	GTGCTGACCCAGTTCGTTGCTCTGCTGGTGGTACGACAGCTTCGTTCCAGCGCGAA	196	
O	y	121	GAGATAGCGCAGTTTGGGCGCGCAGTAGCTGGGCTGGACACACGAGCTGGCCTTCTCTCGT	180	

http://www.genoscope.cns.fr/cdna?s=CSODF011CF12QPI&c=5104.r.

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/note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 82.2%; Score 476; DB 5; Length 957;
Best Local Similarity 86.2%; Pred. No. 1.1e-98;
Matches 579; Conservative 0; Mismatches 0; Indels 93; Gaps 1;
QY 1 ATGCAGTGGCGCGTGGCGCGGCTGGCGGTGGCGCGGCTGGCTCTGCTCTGCTCTGCTCTGCGAGCG 60
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43 ATGCAGTGGCGCGTGGCGCGGCTGGCGGTGGCGCGGCTGGCTCTGCTCTGCTCTGCGAGCG 102
QY 61 GTGCTGACCCAGGTCTGCTGGCTCTGGCTGGGTGGGTAGCAGAGCTTCGTCTTCCAGCGCGAA 120
Db |||||||
103 GTGCTGACCCAGGTCTGCTGGCTCTGGCTGGGTGGGTAGCAGAGCTTCGTCTTCCAGCGCGAA 162
QY 121 GAGATAGCCAGTTGGCGCGGAGTACGCTGGGCTGGACACGAGCTGGCCCTTCTCTCGT 180
Db |||||||
163 GAGATAGCCAGTTGGCGCGGAGTACGCTGGGCTGGACACGAGCTGGCCCTTCTCTCGT 222
QY 181 CTGATCGTGAGCTGGCGCGGCTGACACCCAGGCCACGTGCTGCCGCCACGAGAGCTGCAG 240
Db |||||||
223 CTGATCGTGAGCTGGCGCGGCTGACACCCAGGCCACGTGCTGCCGCCACGAGAGCTGCAG 282
QY 241 TGGGTGTTTGTGATGGGGTGGCTGGATGGGGCGCATGTGCCCTTCTGCACGCCCTGCTG 300
Db |||||||
283 TGGGTGTTTGTGATGGGGTGGCTGGATGGGGCGCATGTGCCCTTCTGCACGCCCTGCTG 342
QY 301 TCCGAGTATGTGCTGCTTCCGGCACCGCTTGGGCTCCCGCGGCCACTCG----- 351
Db |||||||
343 TCCGAGTATGTGCTGCTTCCGGCACCGCTTGGGCTCCCGCGGCCACTCGGGGGCGCTAC 402
QY 352 ----- 351
Db 403 TGGGCTGAGATCTCGGATACCATCATCTCTGGCACCTTCCACCAGTGGAGAGGGGCACC 462
QY 352 -----GGGAGACGGTAGTACACGGGCTGTGAGGCAACA 387
Db 463 ACCAAAGTGAGTCTTTTACCAGGGGAGCGGTAGTACACGGGCTGTGAGGCAACA 522
QY 388 GCTGTGGAGTGGGGGCCAAACACATGGATGGTGGAGTACGGCCGGGGCGGTCAATCCCATCC 447
Db |||||||
523 GCTGTGGAGTGGGGGCCAAACACATGGATGGTGGAGTACGGCCGGGGCGGTCAATCCCATCC 582
QY 448 ACCCTGGCCTTCGCGTGGCCGACACTGTCTTCAGCACCCAGAGCTTCCTCACCCCTCTTC 507
Db |||||||
583 ACCCTGGCCTTCGCGTGGCCGACACTGTCTTCAGCACCCAGAGCTTCCTCACCCCTCTTC 642
QY 508 TATACCTTCGCTTCCTATGCTCGGGGCTTCGGGCTTGAGCTACCACTACCTCTTTGGC 567
Db |||||||
643 TATACCTTCGCTTCCTATGCTCGGGGCTTCGGGCTTGAGCTACCACTACCTCTTTGGC 702
QY 568 CAGGACCCCTTGA 579
Db |||||||
703 CAGGACCCCTTGA 714

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:28:08 ; Search time 167 Seconds
(without alignments)
444.659 Million cell updates/sec

Title: US-09-823-069A-2
Perfect score: 1016
Sequence: 1 MQWAGRRWAALLAVAA.....RSVARGRLRLTYLFGQDP 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseq1990s:*
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4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	990.5	97.5	223	2	Ray03755 Human sig
3	990.5	97.5	223	3	Aab19077 Amino aci
4	990.5	97.5	223	7	Ades4607 Human pro
5	990.5	97.5	223	8	Abm81032 Tumour-as
6	934.5	92.0	223	7	Ades4605 Rat Prote
7	925	91.0	192	4	Aau09155 Mouse sig
8	827.5	81.4	195	3	Aab58747 Breast an
9	544	53.5	106	5	Abb08121 Human NS
10	212.5	20.9	222	2	Adk65615 Yeast C8-
11	212.5	20.9	222	7	Adn19249 Bacterial
12	212.5	20.9	222	8	Adn19490 Bacterial
13	206	20.3	219	8	Adn21450 Bacterial
14	204	20.1	285	8	Adn24370 Bacterial
15	180	17.7	259	8	Adq96108 T cell ac
16	91.5	9.0	395	8	Adq96216 T cell ac
17	91.5	9.0	395	8	Aab93553 Human pro
18	88	8.7	442	4	Abm81907 Tumour-as
19	88	8.7	442	8	Aam93876 Human pol
20	86.5	8.5	414	4	Adl31958 Human pro
21	86.5	8.5	414	4	Abp57482 Mycobacte
22	86	8.5	471	6	Aar47338 Peptide f
23	83	8.2	194	2	Aam51707 Mouse TRP
24	83	8.2	1157	5	Aam51707 Mouse TRP
25	83	8.2	1158	4	Aab86166 Mouse MTR

26	83	8.2	1158	4	AAB86164	Aab86164 Mouse MTR
27	83	8.2	1158	5	ABR83854	Abbr83854 Mouse ltr
28	83	8.2	1158	8	ADR87163	Adr87163 Mouse bet
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31	81.5	8.0	441	6	ADA34139	Ada34139 Acinetoba
32	81.5	8.0	487	6	ADA35480	Ada35480 Acinetoba
33	81.5	8.0	523	8	ADS23855	Ads23855 Bacterial
34	81	8.0	442	4	AAB95029	AbO95029 Human pro
35	81	8.0	463	7	ABO70635	AbO70635 Pseudomon
36	81	8.0	630	4	AAB83244	AbB83244 Human FAT
37	80.5	7.9	211	3	AAG05169	Aag05169 Arabidops
38	80.5	7.9	323	3	AAG05168	Aag05168 Arabidops
39	80.5	7.9	353	4	AEO93119	Aeo93119 Soybean a
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44	79	7.8	330	4	ABG67521	Abg67521 Amino aci
45	78.5	7.7	469	8	ADS27918	Ads27918 Bacterial

ALIGNMENTS

RESULT 1
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ID AAU09154 standard; protein; 192 AA.
XX
AC AAU09154;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human sigma 1 receptor splice variant, sigma1beta.
XX
XX Human; sigma 1 receptor; sigma1beta; tumour imaging; cancer;
KW cell proliferation disorder; tumour; diagnostic; cycostatic.
XX
OS Homo sapiens.
XX
PN WO200174297-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US010650.
XX
PR 31-MAR-2000; 2000US-0193694P.
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(UYWA-) UNIV WAKE FOREST.
XX
PA Wheeler KT, Mach RH, Childers S, Shelness G, Wang L;
PI
XX
DR WPI; 2001-662943/76.
N-PSDB; AAS15569.
XX
PT Novel isolated polynucleotide encoding sigma1beta receptor useful in
screening assay to identify ligands specific for the sigma1beta receptor
for tumor imaging, diagnostic and treatment methods.
XX
PS Claim 9; Fig 2; 56pp; English.
XX
CC The invention relates to an isolated polynucleotide (I) encoding sigma 1
receptor splice variant isolated from mouse adenocarcinoma cells and
human breast tumour cells (I) or the encoded protein (II) is useful for
screening compounds useful in the imaging and treatment of proliferative
masses (i.e. tumours) and in the non-invasive diagnosis of cancer,
comprising (I), or (II) is useful in screening assays to identify ligands
specific for the sigma 1 receptor, and identification of the sigma 1
receptor permits the design of tumour imaging, diagnostic and treatment
methods. (I) is useful for preparing (II), which is useful as immunogen
for making antibodies. These antibodies are useful for a variety of
diagnostic and imaging purposes. Sigma 1 ligands obtained from screening

CC are useful as diagnostic compounds for imaging of, for example, tumour
CC cells, for determining the proliferative status of the tumour, and as
CC therapeutics for the treatment of cancer and other disorders of cell
CC proliferation. The present sequence represents the amino acid sequence of
CC human sigma 1 receptor splice variant, sigma1beta, as described in the
CC invention
XX
SQ Sequence 192 AA;

Query Match 100.0%; Score 1016; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 1.3e-104;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQWAVGRWMAALLLAVAAVLTVVWLWLGTSQSFVQREETIAQLARQVAGLDHLEAFSR 60
DB 1 MQWAVGRWMAALLLAVAAVLTVVWLWLGTSQSFVQREETIAQLARQVAGLDHLEAFSR 60
QY 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSYVLLFGTALSGRHSGET 120
DB 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSYVLLFGTALSGRHSGET 120
QY 121 VVHGPGEATAVWGPNMTVMVEYGRGVPSTLAFALADTVFSTQDFLTFLTYLRSYARGLR 180
DB 121 VVHGPGEATAVWGPNMTVMVEYGRGVPSTLAFALADTVFSTQDFLTFLTYLRSYARGLR 180
QY 181 LELTYLFGQDP 192
DB 181 LELTYLFGQDP 192

RESULT 2
AAY03755
ID AAY03755 standard; protein; 223 AA.
AC AAY03755;
XX
DT 10-JUN-1999 (first entry)
XX
DE Human sigma receptor (SIGR) polypeptide.
XX
KW Sigma receptor; SIGR; vesicle-trafficking disorder; gastrointestinal;
KW inflammatory; immunological disorder; AIDS; arthritis; infection; cancer;
KW neoplastic disorder.
XX
OS Homo sapiens.
XX
PN US5863766-A.
XX
PD 26-JAN-1999.
XX
PF 12-SEP-1997; 97US-00928612.
XX
PR 12-SEP-1997; 97US-00928612.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Corley NC, Hillman JL, Shah P;
XX
PI WPI; 1999-253089/21.
XX
DR N-PSDB; AAX29478.
XX

XX New DNA encoding human sigma receptor polypeptide - useful for treating
PT or preventing vesicle-trafficking, immunological and neoplastic
PT disorders.
XX
XX Claim 1; Fig 1A-D; 28pp; English.

XX This represents a human sigma receptor (SIGR) polypeptide. Host cells
CC containing a vector comprising the SIGR nucleic acid are used for the
CC recombinant expression of the protein. Recombinant SIGR can be used to
CC treat or prevent vesicle-trafficking disorders, e.g. cystic fibrosis,
CC glucose-galactose malabsorption syndrome, hypercholesterolemia, diabetes
CC insipidus, hyper- and hypoglycemia, Grave's disease, goiter, Cushing's

CC disease, and Addison's disease; gastrointestinal disorders (ulcerative
CC colitis, gastric and duodenal ulcers); and other conditions associated
CC with abnormal vesicle trafficking (e.g. hay fever, urticaria (hives),
CC inflammatory bowel disease, myasthenia gravis, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, toxic shock syndrome, and traumatic tissue
CC damage). SIGR can be used to treat or prevent immunological disorders
CC such as AIDS, adult respiratory distress syndrome, allergies, anemia,
CC asthma, atherosclerosis, bronchitis, cholecystitis, atopic dermatitis,
CC Crohn's disease, dermatomyositis, diabetes mellitus, glomerulonephritis,
CC gout, hyperesoinophilia, lupus erythematosus, multiple sclerosis,
CC myasthenia gravis, myocardial or pericardial inflammation, rheumatoid
CC arthritis, osteoarthritis, osteoporosis, pancreatitis, polymyositis,
CC scleroderma, Sjogren's syndrome, Werner syndrome, autoimmune thyroiditis;
CC complications of cancer, hemodialysis, and extracorporeal circulation; and
CC PARIG may also be used to treat or prevent neoplastic disorders e.g.
CC adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma,
CC teratocarcinoma, and cancers of the adrenal gland, bladder, ganglia,
CC gastrointestinal tract, heart, breast, cervix, liver, lung, muscle,
CC ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin,
CC spleen, testis, thymus, thyroid, and uterus
XX
SQ Sequence 223 AA;

Query Match 97.5%; Score 990.5; DB 2; Length 223;
Best Local Similarity 86.1%; Pred. No. 1.1e-101;
Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQWAVGRWMAALLLAVAAVLTVVWLWLGTSQSFVQREETIAQLARQVAGLDHLEAFSR 60
DB 1 MQWAVGRWMAALLLAVAAVLTVVWLWLGTSQSFVQREETIAQLARQVAGLDHLEAFSR 60
QY 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSYVLLFGTALSGRHS --- 117
DB 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSYVLLFGTALSGRHSGRY 120
QY 118 -----GETVHGPGEATAVWGPNMTVMVEYGRGVIPS 149
DB 121 WAETSDTIISGTFHOWREGTTKSEVFPGETVHGPGEATAVWGPNMTVMVEYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFLTFLTYLRSYARGLRLELTLYLFGQDP 192
DB 181 TLAFALADTVFSTQDFLTFLTYLRSYARGLRLELTLYLFGQDP 223

RESULT 3
AAB19077
ID AAB19077 standard; protein; 223 AA.
XX
AC AAB19077;
XX
DT 08-FEB-2001 (first entry)
XX
DE Amino acid sequence of a human sigma receptor binding protein.
XX
KW Human; sigma receptor binding protein; SRBP; cellular marker;
KW breast cancer; HSI; human steroid isomerase.
XX
OS Homo sapiens.
XX
PN WO200057188-A2.
XX
PD 28-SEP-2000.
XX
PF 14-MAR-2000; 2000WO-FR000607.
XX
PR 19-MAR-1999; 99FR-00003418.
XX
PA (SNFI) SANOFI-SYNTHELABO.
XX
PI Casellas P, Simony-Lafontaine J;
XX
XX WPI; 2000-594612/56.
DR

XX Diagnostic composition for detecting breast cancer, useful for predicting
PT response to treatment, contains signal receptor binding protein and/or
PT human sterol isomerase.

XX Example; Fig 4; 27pp; French.

XX The present sequence represents a human signal receptor binding protein
CC (SRBP). The protein is a cellular marker, which may be used in the
CC compositions of the invention. The specification describes a diagnostic
CC composition for detecting breast cancer. The compositions comprises a
CC cellular marker, a protein that has at least 40% homology (at the amino
CC acid level) with SRBP and/or a protein that has at least 40% analogy with
CC HSI (human sterol isomerase). The compositions, or a similar composition
CC containing antibodies specific SRBP and/or HSI, is used to detect breast
CC cancer, whether hormone dependent or not. Analysis of the distribution of
CC the two markers can be used to predict responses to treatment, including
CC identification of patients at high risk of relapse or those who could
CC benefit from auxiliary treatments

XX Sequence 223 AA;

Query Match 97.5%; Score 990.5; DB 3; Length 223;
Best Local Similarity 86.1%; Pred. No. 1.1e-101;
Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
QY 1 MQWAGRRWAAALLLAAVAALTVQVWMLGTQSFVQREIEIAQLARQYAGLDHLEAFSR 60
DB 1 MQWAGRRWAAALLLAAVAALTVQVWMLGTQSFVQREIEIAQLARQYAGLDHLEAFSR 60
QY 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHS--- 117
DB 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHSGRY 120
QY 118 -----GETVVHGPGEATAVEWGPNTMVMVEYGRGVIPS 149
DB 121 WABISDTIISGTFHQWREGTKSEVFPGETVHVGPEATAVEWGPNTMVMVEYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFLTFLFYTLRSYARGLRLELTLYLFGQDP 192
DB 181 TLAFALADTVFSTQDFLTFLFYTLRSYARGLRLELTLYLFGQDP 223

RESULT 4
ADE54607
ID ADE54607 standard; protein; 223 AA.

XX ADE54607;

XX 29-JAN-2004 (first entry)

XX Human Protein NP_005857, SEQ ID NO 412.

XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX W02003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GCHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

XX GENBANK; NP_005857.

PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. Gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 223 AA;

Query Match 97.5%; Score 990.5; DB 7; Length 223;
Best Local Similarity 86.1%; Pred. No. 1.1e-101;
Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

QY 1 MQWAGRRWAAALLLAAVAALTVQVWMLGTQSFVQREIEIAQLARQYAGLDHLEAFSR 60

DB 1 MQWAGRRWAAALLLAAVAALTVQVWMLGTQSFVQREIEIAQLARQYAGLDHLEAFSR 60

QY 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHS--- 117

DB 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHSGRY 120

QY 118 -----GETVVHGPGEATAVEWGPNTMVMVEYGRGVIPS 149

DB 121 WABISDTIISGTFHQWREGTKSEVFPGETVHVGPEATAVEWGPNTMVMVEYGRGVIPS 180

QY 150 TLAFALADTVFSTQDFLTFLFYTLRSYARGLRLELTLYLFGQDP 192

DB 181 TLAFALADTVFSTQDFLTFLFYTLRSYARGLRLELTLYLFGQDP 223

RESULT 5

ABM81032

ID ABM81032 standard; protein; 223 AA.

XX ABM81032;

XX 18-NOV-2004 (first entry)

XX Tumour-associated antigenic target (TAT) polypeptide PRO36808, SEQ:2671.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;

XX tumour; diagnosis; cell proliferative disorder; breast cancer;

XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX Homo sapiens.
OS
XX
XX
PN WO2004030615-A2.
XX
XX
PD 15-APR-2004.
XX
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
XX
PA (GETH) GENENTECH INC.
XX
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
XX
DR WPI; 2004-347921/32.
DR N-PSDB; ACN38882.
XX
XX
PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX
PS Claim 12; SEQ ID NO 2671; 7273pp; English.
XX
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
XX
SQ Sequence 223 AA;
Query Match 97.5%; Score 990.5; DB 8; Length 223;
Best Local Similarity 86.1%; Pred. No. 1.1e-101;
Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
QY 1 MQWAVGRWAWAALLLAVAAVLTVVWMLGTQSFVQREETAQLARQVAGLDHELAFSR 60
DB 1 MQWAVGRWAWAALLLAVAAVLTVVWMLGTQSFVQREETAQLARQVAGLDHELAFSR 60
QY 61 LIVELRRLHPGHVLPDEELQWVFNAGGWMGACLLHASLSYVLLFGTALGSRGHS--- 117
DB 61 LIVELRRLHPGHVLPDEELQWVFNAGGWMGACLLHASLSYVLLFGTALGSRGHSGRY 120
QY 118 -----GETVHGPGEATAVEMGPNMTVMVYGRGVIPS 149
DB 121 WAEISDTIISCTFHQWREGTKSEVPYCGTETHVHGEATAVEMGPNMTVMVYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFLTLYTLRSYARGRLLELTLYLFGQDP 192
DB 181 TLAFALADTVFSTQDFLTLYTLRSYARGRLLELTLYLFGQDP 223

RESULT 6
ADE54605
ID ADE54605 standard; protein; 223 AA.
XX
XX ADE54605;
AC
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAD01198, SEQ ID NO 410.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
OS
XX
PN WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
PF
XX
XX 14-AUG-2001; 2001US-0312147P.
PR
XX 01-NOV-2001; 2001US-0346382P.
PR
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR
XX
XX GENBANK; AAD01198.
PT
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
PS
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (shown in Table 2 of
XX the specification) which is differentially expressed during pain. Note:
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 223 AA;
Query Match 92.0%; Score 934.5; DB 7; Length 223;
Best Local Similarity 79.8%; Pred. No. 1.9e-95;
Matches 178; Conservative 4; Mismatches 10; Indels 31; Gaps 1;
QY 1 MQWAVGRWAWAALLLAVAAVLTVVWMLGTQSFVQREETAQLARQVAGLDHELAFSR 60

Db 1 MPWAGRRWAWITLFTITVAVLQAVWMLGTQSFVQREETIAQLARQVAGLDHLEAFSR 60
61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHS 117
61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHSRY 120
118 -----GETVVHGPGEATAVWGPNMTVMVEYGRGVIPS 149
121 WAEISDTISGTHQWREGTKSEVYYPGETVVHGPGEATDVWGPNMTVMVEYGRGVIPS 180
150 TLAPALADTVFSTQDFLTFLTYLRSYARGRLRLBELTTLVFGQDP 192
181 TLAFALSDTIFSTQDFLTFLTYLRSYARGRLRLBELTTLVFGQDP 223

RESULT 7
AAU09155
ID AAU09155 standard; protein; 192 AA.

AC AAU09155;
XX
XX
DT 29-JAN-2002 (first entry)
XX Mouse sigma 1 receptor splice variant, sigma1beta.
XX
XX Mouse; sigma 1 receptor; sigma1beta; tumour imaging; cancer;
KW cell proliferation disorder; tumour; diagnostic; cytostatic.
XX
XX Mus sp.

XX WQ200174297-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US010650.
XX
XX 31-MAR-2000; 2000US-0193694P.
XX
XX (UYWA-) UNIV WAKE FOREST.

XX Wheeler KT, Mach RH, Childers S, Shelness G, Wang L;
XX
XX WPI; 2001-662943/76.
XX N-PSDB; AAS15570.

XX Novel isolated polynucleotide encoding sigma1beta receptor useful in
XX screening assay to identify ligands specific for the sigma1beta receptor
XX for tumor imaging, diagnostic and treatment methods.

XX Claim 21; Fig 4; 56pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding sigma 1
XX receptor splice variant isolated from mouse adenocarcinoma cells and
XX human breast tumour cells. (I) or the encoded protein (II) is useful for
XX screening compounds useful in the imaging and treatment of proliferative
XX masses (i.e. tumours) and in the non-invasive diagnosis of cancer,
XX preferably in the diagnosis of proliferative cancer cells. (II), a cell
XX comprising (I), or (II) is useful in screening assays to identify ligands
XX specific for the sigma 1 receptor, and identification of the sigma 1
XX receptor permits the design of tumour imaging, diagnostic and treatment
XX methods. (I) is useful for preparing (II), which is useful as immunogen
XX for making antibodies. These antibodies are useful for a variety of
XX diagnostic and imaging purposes. Sigma 1 ligands obtained from screening
XX are useful as diagnostic compounds for imaging of, for example, tumour
XX cells, for determining the proliferative status of the tumour, and as
XX therapeutics for the treatment of cancer and other disorders of cell
XX proliferation. The present sequence represents the amino acid sequence of
XX mouse sigma 1 receptor splice variant, sigma1beta, as described in the
XX invention

XX Sequence 192 AA;

Query Match 91.0%; Score 925; DB 4; Length 192;
Best Local Similarity 89.0%; Pred. NO. 1.8e-94;
Matches 170; Conservative 7; Mismatches 14; Indels 0; Gaps 0;
QY 1 MOWAVGRRWAWALLLAVAAVLTVVWMLGTQSFVQREETIAQLARQVAGLDHLEAFSR 60
DB 1 MPWAGRRWAWITLFTITVAVLQAVWMLGTQSFVQREETIAQLARQVAGLDHLEAFSR 60
QY 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHSGET 120
DB 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHSGET 120
QY 121 VVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAPALADTVFSTQDFLTFLTYLRSYARGRLR 180
DB 121 VVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAPALADTVFSTQDFLTFLTYLRSYARGRLR 180
QY 181 LELTTLVFGQD 191
DB 181 LELTTLVFGQD 191

RESULT 8
AAB58747
ID AAB58747 standard; protein; 195 AA.

AC AAB58747;
XX
XX 27-MAR-2001 (first entry)

XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 455.
XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neurotropic; neurprotection; antiviral; antiallergic; hepatotropic;
KW antidiabetic; antiinflammatory; antiulcer; vulnery; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.

XX Homo sapiens.

XX WQ200055173-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005881.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

XX N-PSDB; AAF21650.

XX New human breast and ovarian cancer associated gene sequences and the
XX polypeptides encoded by these genes, useful in the prevention, treatment
XX and diagnosis of cancer, immune disorders, cardiovascular disorders and
XX neurological diseases.

XX Claim 11; Page 883-884; 1299pp; English.

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
XX proteins AAB58711 - AAB59128. The DNA and protein sequences are
XX associated with breast and ovarian cancer. Included in the invention are
XX sequences AAF22032 - AAF22040 and AAB59129 which are used in the
XX isolation and characterisation of the DNA and protein sequences of the
XX invention. The breast and ovarian cancer associated DNA, protein, agonist
XX or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic;
XX neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
XX antiinflammatory; antiulcer; vulnery; anticonvulsant; antibacterial;

CC antifungal; antiparasitic and cardiant activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and agonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX
 XX Sequence 195 AA;

Query Match 81.4%; Score 827.5; DB 3; Length 195;
 Best Local Similarity 83.9%; Pred. No. 1.4e-83;
 Matches 162; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
 QY 31 GTQSFVQREETAQLARQAGLDHDLAFSLRLVLRLLHPGHVLPDEELQWVFNAGGWM 90
 DB 3 GTQSFVQREETAQLARQAGLDHDLAFSLRLVLRLLHPGHVLPDEELQWVFNAGGWM 62
 QY 91 GAMCLLHASLSYVLLFGTALSGRHS-----GE 119
 DB 63 GAMCLLHASLSYVLLFGTALSGRHSGRYWAIEISDTISGTFHQWREGTKSEVFPGE 122
 QY 120 TVVHGPGETAWEVGPNTWVYGRGVIPSTLAFALADTVFSTQDPLFTYTLRSYARGL 179
 DB 123 TVVHGPGETAWEVGPNTWVYGRGVIPSTLAFALADTVFSTQDPLFTYTLRSYARGL 182
 QY 180 RLELTTYLFGQDP 192
 DB 183 RLELTTYLFGQDP 195

RESULT 9
 ABB06121
 ID ABB06121 standard; protein; 106 AA.
 AC ABB06121;
 XX
 XX 10-MAY-2002 (first entry)
 XX
 XX Human NS protein sequence SEQ ID NO:213.
 XX
 KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotropic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
 KW anticonvulsant; antidiabetic; tranquiliser; antidepressant; neuroleptic;
 KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
 KW gastrointestinal; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW contractective; degenerative disease; multiple sclerosis; psoriasis;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW infertility; cardiovascular disease; coagulation disease; hypertension;
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200206315-A2.
 XX
 XX 24-JAN-2002.
 XX
 XX 17-JUL-2001; 2001WO-IL000653.
 XX
 XX 18-JUL-2000; 2000IL-00137345.
 XX
 XX 15-DEC-2000; 2000IL-00140354.
 XX
 XX (COMP-) COMPUGEN LTD.
 XX

PI Mintz L, Freilich S, Bernstein J;
 XX WPI; 2002-155037/20.
 DR N-PSDB; ABL39775.
 XX
 PT One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's.
 XX
 PS Claim 6; Page 248; 290pp; English.
 XX
 XX ABL39691 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antirheumatic, antiarthritic, antipsoriatic, ophthalmological, virucide,
 CC vasotropic, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular, cardiant,
 CC anticoagulant, antifibrinolytic, antidiabetic, antiasthmatic, antiulcer,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquiliser, antiulcer,
 CC antidepressant, gastrointestinal, neuroleptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisenese therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive
 XX
 SQ Sequence 106 AA;

Query Match 53.5%; Score 544; DB 5; Length 106;
 Best Local Similarity 98.1%; Pred. No. 2.4e-52;
 Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MCWAVGRWAWAALLLAVAALVTQVWLWLTQSFVQREETAQLARQAGLDHDLAFSR 60
 DB 1 MCWAVGRWAWAALLLAVAALVTQVWLWLTQSFVQREETAQLARQAGLDHDLAFSR 60
 QY 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSSEYVL 105
 DB 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSSEYVL 105
 RESULT 10
 AAR90670
 ID AAR90670 standard; protein; 222 AA.
 XX AAR90670;
 XX
 XX 25-MAR-2003 (revised)
 XX 11-JUL-1996 (first entry)
 XX
 XX S. cerevisiae delta 8-7 isomerase.
 DE
 XX Delta 8-7 isomerase; sterol; biosynthesis; accumulation; composition;
 KW modulation; mutant; yeast; enzyme.
 XX
 XX Saccharomyces cerevisiae.
 OS
 XX US5480805-A.
 XX
 XX 02-JAN-1996.
 XX
 XX 10-MAY-1994; 94US-00240496.
 XX
 XX 12-AUG-1992; 92US-00929764.
 XX
 XX (STAD) AMOCO CORP.
 XX
 XX Wolf FR, Cuellar RE;

XX WPI; 2004-061375/06.
DR
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX
PS Claim 1; SEQ ID NO 1902; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 222 AA;
Query Match 20.9%; Score 212.5; DB 8; Length 222;
Best Local Similarity 30.0%; Pred. No. 5.3e-15; Mismatches 66; Indels 43; Gaps 8;
Matches 62; Conservative 36;
QY 14 LLLAAVAALTVQVW-LWLGTQSFVFOREIAQLARQYAGLDHE---LAFSLRILVELRLH 69
DB 8 LLIGVGVYIMVFLTWLPT-NYMPDPKTLNEICNSVISKHNAEGLSTDLQVDRDL 66
QY 70 PGHVLDPDEL-----QWVFVAGGMMGAMCLLHLSLSEYVLLFGTALSGRHSSE---- 119
DB 67 ASH-YGDEYINRYVKEEWFNNAGGANGQMILHASVSEYLLIFGTAVGTEGHTGVHFD 125
QY 120 ---TVVHG-----PGEATAVEWG-----PNTMMVEYGRGVIPSTILA 152
DB 126 DYFTILHGTQIAALPYATAEYVTPGWTTHLKKYAKQYSGPGGSPALSLAQWIPCMPLP 185
QY 153 FALADTVFSTQDFLTLFYTLRSYARGL 179
DB 186 FGFLDTFSSTLDLYTLRYVTLTARDM 212
RESULT 13
ADN19490
ID ADN19490 standard; protein; 219 AA.
XX
AC ADN19490;
XX
XX 02-DEC-2004 (first entry)
XX
XX Bacterial polypeptide #2143.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;

KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 2143; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 219 AA;
Query Match 20.3%; Score 206; DB 8; Length 219;
Best Local Similarity 32.9%; Pred. No. 2.7e-14; Mismatches 52; Indels 38; Gaps 4;
Matches 55; Conservative 22;
QY 39 REEIAQLARQYAGLDHELAFAFSLRILVELRLHGHVLPDEELQWVFVAGGMMGAMCLLHA 98
DB 42 KQSIALYANDTKALLYDLS-DRLVAEYGDL-----ITPVNQDEWHNNAGGANGTWFILHA 96
QY 99 SLSEYVLLFGTALSGRHS-----ETVHGPGGATAVEWGP 135
DB 97 SPSEYLIFFGTPIGTGEGSHGVHMADDYFTILRGLAASANDLEARVLPDQGHVHPWGH 156
QY 136 NT-----WMVEYGRGVIPSTILAFAALADTVFSTQDFLTLFYTL 172
DB 157 TQAYSMPSGPEPCFALELAQGMIVSMLDPFGMDGLFSTIDFGLYLKTIV 203
RESULT 14

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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:41:20 ; Search time 42 Seconds
(without alignments)
341.253 Million cell updates/sec

Title: US-09-823-069A-2
Perfect score: 1016
Sequence: 1 MQMVGRRWAAALLAVAA.....RSVARGRLLELTTLFGQDP 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/prodata/1/iaa/6CTUS COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	990.5	97.5	223	2	US-08-928-612-1
2	918.5	90.4	223	2	US-08-928-612-3
3	212.5	20.9	222	1	US-08-240-496A-2
4	83.5	8.2	238	4	US-09-502-540-15642
5	83	8.2	194	1	US-08-063-552-8
6	83	8.2	194	5	PCT-US93-05704-8
7	82	8.1	1045	4	US-09-252-991A-17661
8	81.5	8.0	441	4	US-09-328-352-5426
9	81.5	8.0	487	4	US-09-328-352-6767
10	81	8.0	463	4	US-09-252-991A-19381
11	80.5	7.9	353	3	US-09-461-474-4
12	80.5	7.9	494	4	US-09-252-991A-32227
13	77	7.6	317	4	US-09-489-039A-10526
14	76.5	7.5	705	4	US-09-328-352-4457
15	76	7.5	376	4	US-09-252-991A-23396
16	75.5	7.4	509	4	US-09-270-767-41638
17	74.5	7.3	623	4	US-09-252-991A-19867
18	74	7.3	162	4	US-09-502-540-11988
19	74	7.3	480	4	US-09-252-991A-18961
20	73.5	7.2	252	4	US-09-328-352-7284
21	73.5	7.2	295	4	US-09-252-991A-20718
22	73.5	7.2	551	4	US-09-489-039A-14227
23	73.5	7.2	1165	4	US-09-949-016-6874
24	73	7.2	295	4	US-09-583-110-3181
25	73	7.2	323	4	US-09-107-433-3410
26	73	7.2	335	4	US-09-602-787A-518
27	73	7.2	398	4	US-09-252-991A-19152

28	73	7.2	527	4	US-09-602-787A-516	Sequence 516, App
29	72.5	7.1	391	4	US-09-543-681A-7029	Sequence 7029, Ap
30	72.5	7.1	1165	4	US-09-949-016-11392	Sequence 11392, A
31	72.5	7.1	7257	3	US-09-335-409-5	Sequence 5, Appli
32	72.5	7.1	7257	3	US-09-568-102-5	Sequence 5, Appli
33	72.5	7.1	7257	3	US-09-567-963-5	Sequence 5, Appli
34	72.5	7.1	7257	3	US-09-568-480-5	Sequence 5, Appli
35	72.5	7.1	7257	3	US-09-568-486-5	Sequence 5, Appli
36	72.5	7.1	7257	3	US-09-568-472-5	Sequence 5, Appli
37	72.5	7.1	7257	3	US-09-567-899-5	Sequence 5, Appli
38	71.5	7.0	178	4	US-09-543-681A-7183	Sequence 7183, Ap
39	71.5	7.0	460	4	US-09-252-991A-24308	Sequence 24308, A
40	71.5	7.0	1996	2	US-08-804-227C-9	Sequence 9, Appli
41	71.5	7.0	1996	2	US-08-804-198-3	Sequence 3, Appli
42	71	7.0	373	4	US-09-622-439-6	Sequence 6, Appli
43	71	7.0	373	4	US-09-622-439-26	Sequence 26, Appli
44	71	7.0	373	4	US-10-318-142-6	Sequence 6, Appli
45	71	7.0	373	4	US-10-318-142-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-08-928-612-1
; Sequence 1, Application US/08928612
; Patent No. 5863766
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN SIGMA RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,612
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0383 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PROSTUT04
; CLONE: 1542751
; US-08-928-612-1
Query Match 97.5%; Score 990.5; DB 2; Length 223;
Best Local Similarity 86.1%; Pred. No. 4e-106;

Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;
QY 1 MQWAVGRRWAAALLLAAVAVLTQVWVLWGTSQVFFQREETAQLARQVAGLDHLEAFSR 60
Db 1 MQWAVGRRWAAALLLAAVAVLTQVWVLWGTSQVFFQREETAQLARQVAGLDHLEAFSR 60
QY 61 LIVELRRLLHPGHVLPDEELQWVFNAGGMMGAMCLLHASLSYVLLFGTALGSRGHS--- 117
Db 61 LIVELRRLLHPGHVLPDEELQWVFNAGGMMGAMCLLHASLSYVLLFGTALGSRGHSRY 120
QY 118 -----GETVVHGPGEATAVEMGPNMTMMVEYGRGVIPS 149
Db 121 WAEISDTIISGTFHQWREGTTKSEVFPYPGETVVHGPGEATAVEMGPNMTMMVEYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFLFTFYTLRSYARGRLRLLELTYYLFGQDP 192
Db 181 TLAFALADTVFSTQDFLFTFYTLRSYARGRLRLLELTYYLFGQDP 223

RESULT 2
US-08-928-612-3
; Sequence 3, Application US/08928612
; Patent No. 5863766
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN SIGMA RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/928,612
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0383 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1403300
US-08-928-612-3

Query Match 90.4%; Score 918.5; DB 2; Length 223;
Best Local Similarity 79.4%; Pred. No. 8.2e-98;
Matches 177; Conservative 4; Mismatches 11; Indels 31; Gaps 1;
QY 1 MQWAVGRRWAAALLLAAVAVLTQVWVLWGTSQVFFQREETAQLARQVAGLDHLEAFSR 60
Db 1 MQWAVGRRWAAALLLAAVAVLTQVWVLWGTSQVFFQREETAQLARQVAGLDHLEAFSR 60

Db 1 MQWAVGRRWAAALLLAAVAVLTQVWVLWGTSQVFFQREETAQLARQVAGLDHLEAFSK 60
QY 61 LIVELRRLLHPGHVLPDEELQWVFNAGGMMGAMCLLHASLSYVLLFGTALGSRGHS--- 117
Db 61 LIVELRRLLHPGHVLPDEELQWVFNAGGMMGAMCLLHASLSYVLLFGTALGSRGHSRY 120
QY 118 -----GETVVHGPGEATAVEMGPNMTMMVEYGRGVIPS 149
Db 121 WAEISDTIISGTFHQWREGTTKSEVFPYPGETVVHGPGEATAVEMGPNMTMMVEYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFLFTFYTLRSYARGRLRLLELTYYLFGQDP 192
Db 181 TLAFALADTVFSTQDFLFTFYTLRSYARGRLRLLELTYYLFGQDP 223

RESULT 3
US-08-240-496A-2
; Sequence 2, Application US/08240496A
; Patent No. 5480805
; GENERAL INFORMATION:
; APPLICANT: Wolf, Fred R.
; APPLICANT: Cuellar, Richard E.
; TITLE OF INVENTION: Composition for Modulating Sterols in
; TITLE OF INVENTION: Yeast
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Joanne M. Giesser
; STREET: Amoco Corp., Suite 600, 55 Shuman Blvd.
; CITY: Naperville
; STATE: IL
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/240,496A
; FILING DATE: 10-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/929,764
; FILING DATE: 12-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Giesser, Joanne M.
; REGISTRATION NUMBER: 32,838
; REFERENCE/DOCKET NUMBER: 31,456
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (708) 717-2443
; TELEFAX: (708) 717-2430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-240-496A-2

Query Match 20.9%; Score 212.5; DB 1; Length 222;
Best Local Similarity 30.0%; Pred. No. 2.7e-16;
Matches 62; Conservative 36; Mismatches 66; Indels 43; Gaps 8;
QY 14 LLLAAVAVLTQVWV-LWLGTQSFVQREETAQLARQVAGLDHE---LAFSRLLVLELRLH 69
Db 8 LLIGVGVYIMNVLTFTTLPT-NYFDPKTLNEICNSVLSKNAASGLSTEDLLQDVRDAL 66
QY 70 PGHVLVDEEL-----QWVFNAGGMMGAMCLLHASLSYVLLFGTALGSRGHSB----- 119
Db 67 ASH-YGDEYINRYVKEWVFNAGGMMQMIILHASVSEYLLFGTAVGTEGTVGFAD 125

QY 120 ----TUVHG-----PGEATAVEMG-----PNTWMVEYGRGVIPSTIA 152
Db 126 DFTILHGQIAALPYATEAEVVTGTHLKKGYAKQYMPGGSFALELAQWIPCMPL 185
QY 153 FALADTVFSTQDFTLTYLRSYARGL 179
Db 186 FGFLDTFSTLDLYTLTYRTVYLTARDM 212

RESULT 4
US-09-902-540-15642
; Sequence 15642, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: MYXOCOCCUS XANTHUS Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15642
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15642

Query Match 8.2%; Score 83.5; DB 4; Length 298;
Best Local Similarity 27.7%; Pred. No. 0.33; 88; Indels 49; Gaps 11;
Matches 61; Conservative 22; Mismatches 22

QY 4 AVGRRWAAALLAVAAVLTVVWLMLGTQSFVFOR--BEIAQLARQYAGLDHAFS-- 59
Db 33 AVDRVSLAALQA--APESKAPAHHLGT---LLSRAVDPVLSRLHA--ROVALALSCA 87
QY 60 -----RLIVELRLHPGHVLPDEELQWVFN-----AGWGMGA 92
Db 88 QGLPAARALLEQREVLLKRLVPLRIHPSPVFADEVQLALRANLLMPRAEAPSRLLYAGA 147
QY 93 MCLLH---ASLSYVLLFGTALSGRH--SGETVHVGPGGEATAVEMGPNWVEYGRGVIP 148
Db 148 GPILLHWVSISATRLALMRKALGEASHVEAEVLAHPAG--GLELG---FVREEARGHVR 203
QY 149 STLAFALADTVFSTQDFTLTYLRSYARGIRLELTATYLF 188
Db 204 AAFVRAVSLDDEDRLLRLHFVER-----LSLERMGAUF 238

RESULT 5
US-08-063-552-8
; Sequence 8, Application US/08063552
; Patent No. 5688936
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/063,552
; FILING DATE: 19930514
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 9067-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Transposon 10
; US-08-063-552-8

Query Match 8.2%; Score 83; DB 1; Length 194;
Best Local Similarity 29.2%; Pred. No. 0.2;
Matches 38; Conservative 18; Mismatches 42; Indels 32; Gaps 7;

QY 14 LLLAVAAVLTVVWLMLGTQSFVFOREEIAQLARQYAGLDH-ELAFSRLI--VELRRLHP 70
Db 45 VLLALYALMOVIFAPWLGKMSDRFGRPVLLSLIGASLDYLLAFSSALMMLYLGRLLS 104
QY 71 G-----HVLPD-----BELOVFNAGWGMGMCLLHASLSEYVLLFTALGSRG 115
Db 105 GITGATGAASVIADTTTSASQKVKWF-----GWLGSFGLG-----LIAGPIIG--G 150
QY 116 HSGETVHGP 125
Db 151 PAGEISPHSP 160

RESULT 6
PCT-US93-05704-8
; Sequence 8, Application PC/TUS9305704
; GENERAL INFORMATION:
; APPLICANT: Edwards, Robert H
; TITLE OF INVENTION: Vesicle Membrane Transport Proteins
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05704
; FILING DATE: 19930611
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 9067-1PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 796-4000
; TELEFAX: (818) 795-6321
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 194 amino acids
; TYPE: AMINO ACID

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: Transposon 10
PCT-US93-05704-8

Query Match      8.2%; Score 83; DB 5; Length 194;
Best Local Similarity 29.2%; Pred. No. 0.2;
Matches 38; Conservative 18; Mismatches 42; Indels 32; Gaps 7;

QY 14 LLLAAVAVLTQVWMLWLTQSFVFOREEIAQLARQYAGLDH-ELAFSRLI--VELRLRHP 70
DB 45 VLLALYALMQVIFAPWLGKMSDRFGRRPVLLLSLIGASLDYLLAFSALWMLYIGRLLS 104
QY 71 G-----HVLDP-----EELQVFNAGMGMGAMCLLHASLSEVLLFGTALGSRG 115
DB 105 GITGATGAASVIADTTTSASQVRKWF-----GWLGSFGLG-----LIAGPIIG--G 150
QY 116 HSGETVVHVP 125
DB 151 PAGEISPHSP 160

RESULT 7
US-09-252-991A-17661
; Sequence 17661, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17661
; LENGTH: 1045
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17661

Query Match      8.1%; Score 82; DB 4; Length 1045;
Best Local Similarity 32.6%; Pred. No. 2.9;
Matches 42; Conservative 13; Mismatches 50; Indels 24; Gaps 7;

QY 10 ANAALLAV-----AAVLTVVWLW---LGTQSFVFOREEIAQLARQYAGLDH-ELAFSRLI 62
DB 356 SWSALLDALARLGAARVTVQVLLATRAGQDHALGHPHLLARQVGHIERQAAAFQGAR 415
QY 63 VELRLRHPG-HV---LPDEELQVFNAGMGMGAMCLLHASLSEVLL-FGTALGSRGHS 117
DB 416 VGRALDPGEHVTLRVADVQRQ-----AQLVGA-----FDEFALLDQGDQAVDRGES 463
QY 118 GETVVHGP 126
DB 464 VEVDLRGDG 472

RESULT 8
US-09-328-352-5426
; Sequence 5426, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA

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; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5426
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5426

Query Match      8.0%; Score 81.5; DB 4; Length 441;
Best Local Similarity 26.1%; Pred. No. 0.98;
Matches 42; Conservative 27; Mismatches 67; Indels 25; Gaps 8;

QY 40 EEIAQLARQYAGLDH-ELAF-----SRLIVELRLHPGHVLPDEELQVFNAGW 89
DB 232 EGISKITAQDVKYAEELGFRKHLGIARRAEKGIEL-RVHP-TLIPDEQL-----IANVGV 286
QY 90 MGAMCLLHASLSEVLLFGTALGSRGHSGETVVHGPGEATAVEMGPNMTWVYGRGVIPS 149
DB 287 KNAV-LVQANAVGPTLYYGAGAGA-GPTASAVV-----ADVIDIVRDISYTEDGAGTIPQ 339
QY 150 TLAFALADTVFSTQDFLFTYTLRSYAR---GLRLLETTYL 187
DB 340 LAFEALTNPILSREEMTTGYIRLNABDDOTGVLDADVTTIL 380

RESULT 9
US-09-328-352-6767
; Sequence 6767, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6767
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6767

Query Match      8.0%; Score 81.5; DB 4; Length 487;
Best Local Similarity 21.0%; Pred. No. 1.1;
Matches 37; Conservative 30; Mismatches 66; Indels 43; Gaps 7;

QY 13 ALLLAAVAVLTQVWMLWLTQ-----SFVFOREEIAQLARQYAGLDH-ELA 57
DB 33 ATSIGLACFLAVLEWKWLRTQNPYKDLFKYWKIKFAVAFGNGVGVSVVMSYQFGTNWSE 92
QY 58 FSRLLIVELRLRHPGHVLPDEELQVFNAGMGMGAMCLLHASLSEVLLFGTA-LGSRGH 116
DB 93 FSRVAGSI---TGPLLTYEVLSPAFFLEA-GFLG-----IMLFGNGRVPRAH 135
QY 117 SGETVVHGPGEATAVEM--GPNMTWVYGRGVISTLAFALADTVFSTQDFLFTLY 170
DB 136 FFATILMVAIGTCISMFWILSSNMW-----QTPQGFATENGIIIVPKWLAIVF 183

RESULT 10
US-09-252-991A-19381
; Sequence 19381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

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/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 19381
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19381

Query Match
Best Local Similarity 23.3%; Pred. No. 1.2;
Matches 53; Conservative 27; Mismatches 85; Indels 62; Gaps 9;

QY 2 QNVA---GRWAAALLAAVLTQVVMWLTQSFVQREBIAOLA---ROYAGLDHE 55
Db 230 QMLADGGHPAVPATLAVLLASUALVVPAMPETRLAGTPPATLAFRRVLA--DRP 287

QY 56 LAFSRLIVELRLRHGHPVLPDEELQWVFVNAG-----GWMGAMCLLHASLSEY 103
Db 288 LQTRALLVAVLVN-----LVFSFYAAGPFPMVGDLPGLGFGWIGLAIAIAGSLGAL 337

QY 104 V-----LLFGTALSGRHSGETVHVHGPGEATAVWGPNTVMVEYGRGV-IPS 149
Db 338 LNRRLPRTWNSARRVRLGLALAAAGATAQTLLAAVGVAGLYWALPALPIFIFGVAIPN 397

QY 150 TLAFAL-----ADTVFSTQDFLTFLFYTLRSYARGLRLELTLYL 187
Db 398 LLGPALHAYDDCRGAGALFGLAYLLI-----GLGLGASTLL 435

RESULT 11
US-09-461-474-4
/ Sequence 4, Application US/09461474
/ Patent No. 6278042
/ GENERAL INFORMATION:
/ APPLICANT: Allen, Steve
/ APPLICANT: Rafaleki, Antoni
/ APPLICANT: Sakai, Hajime
/ TITLE OF INVENTION: Plant Metal Transporters
/ FILE REFERENCE: BB1303 US NA
/ CURRENT APPLICATION NUMBER: US/09/461,474
/ CURRENT FILING DATE: 1999-12-14
/ EARLIER APPLICATION NUMBER: 60/112,562
/ EARLIER FILING DATE: 1998-12-16
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: Microsoft Office 97
/ SEQ ID NO 4
/ LENGTH: 353
/ TYPE: PRT
/ ORGANISM: Glycine max
US-09-461-474-4

Query Match
Best Local Similarity 24.5%; Pred. No. 0.93;
Matches 34; Conservative 18; Mismatches 58; Indels 29; Gaps 4;

QY 72 HVLDPDELOHVFVNAGWNG-----AMCLLHASLSEYVLLFQT-----ALGSRGHS 117
Db 11 NVLEQETLKWVFGVGKGVKTTCCSILSILLATVRSSVLIISTDPAHNLSDAFQORFTK 70

QY 118 GETVHVHGPGEATAVWGPNTVMVEY-----RCVIP---STLAFALADTVFST 162
Db 71 TPTLVNGFSNLYAMEVDFTVEHEDMGAGDNQDTLFLSELAGAIPIGIDEAMSFAEMLKLVT 130

QY 163 QDFLTFLFYTLRSYARGLR 181
Db 131 MDISVIVDPTAPTGHTRL 149

RESULT 12
US-09-252-991A-32227
/ Sequence 32227, Application US/09252991A

/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 32227
/ LENGTH: 494
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
/ FEATURE:
/ NAME/KEY: UNSURE
/ LOCATION: (139)
/ OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-32227

Query Match
Best Local Similarity 23.0%; Pred. No. 1.5;
Matches 32; Conservative 16; Mismatches 50; Indels 41; Gaps 3;

QY 14 LLLAAVAALVTQVVMWLTQSFVQREBIAOLAQYAGLDHDLAFSLRLIVELRLRHGHPV 73
Db 99 LVVVVLLALLSHVV-----DEALELRMVADLERPHGQV 132

QY 74 LPDEELQWVFVNAGWGMGAMCLLHASLSEYVLLFGTALSGRHSGETVHVHGPGEATAVW 133
Db 133 -----EHVGGVXGVGMARAGHAEVLLAVVEQAQVHAGTVELEGRAEHQGALL 182

QY 134 GPNTWMV-----EYGRGVI 147
Db 183 GRSQVVVAAGVBAQCEGVV 201

RESULT 13
US-09-489-039A-10626
/ Sequence 10626, Application US/09489039A
/ Patent No. 6610836
/ GENERAL INFORMATION:
/ APPLICANT: Gary Breton et. al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
/ TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
/ FILE REFERENCE: 2709.2004001
/ CURRENT APPLICATION NUMBER: US/09/489,039A
/ CURRENT FILING DATE: 2000-01-27
/ PRIOR APPLICATION NUMBER: US 60/117,747
/ PRIOR FILING DATE: 1999-01-29
/ NUMBER OF SEQ ID NOS: 14342
/ SEQ ID NO 10626
/ LENGTH: 317
/ TYPE: PRT
/ ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10626

Query Match
Best Local Similarity 27.7%; Pred. No. 2;
Matches 51; Conservative 20; Mismatches 61; Indels 52; Gaps 11;

QY 22 LQGVVWLTQSFVQREBIAOLAQYAGLDH-----ELAFSLRLIVELRLRHGHPVLPD 76
Db 95 MTQYFSMW-GNLTII---RENLLFIARLYS-LDRRRRVERVALSELGLTARQ----HOLAK 145

QY 77 BELQWVFVNAGWGMGAMCLLHASLSEYVLLF---GTA-----LGSRGHS 117
Db 146 E-----LSGGWKQRMALAAACMLHPVLLFLDEPTAGVDPKARRRFQWMLHQLSDRGIS 198

QY 118 GETVHVHGPGEATAVWGPNTVMVEYGRVIPSTLAFALADTVFSTQDFLTFLFYTLRSYAR 177
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Db 199 LLVSTHYMDEA---RECHKVAVLSYGRLLANGTIA-----SIASQNLI-----TWRTSGA 246
QY 178 GLRL 181
Db 247 GLTL 250

RESULT 14
US-09-328-352-4457
; Sequence 4457, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4457
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4457

Query Match 7.5%; Score 76.5; DB 4; Length 705;
Best Local Similarity 26.4%; Pred. No. 7.2;
Matches 48; Conservative 23; Mismatches 56; Indels 55; Gaps 12;
QY 9 WAAWALLLAAVAVL-----TQVVLWLGTQSFVQREETAQLARQYAGLDHELAFSR 60
Db 23 WSLVAIIIGAISGMLALSERGEHNAVWLVLAAC-----VISIAYRP-----YSLFIAT 71
QY 61 LIVEL--RRLHPGHVLPDEELQWVFVNAGGMMGAMCLLHASLSEYVLLFGTALGSRGHSG 118
Db 72 KVFELNPRELTFAHLAD--GLDYVPTN-----KVV-LFGHHFAAIAGAG 113
QY 119 ETVVHGPGGATAVEGPNP--WVVEYGRGVIPSTLAFALADTVFSTQDFLTFLPYTLRSYAR 177
Db 114 PLV--GPILAAQMGFLPGTILLLV---GVV-----LAGAV---QDFLVLPFISTRDGR 158
QY 178 GL 179
Db 159 SL 160

RESULT 15
US-09-252-991A-23396
; Sequence 23396, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23396
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23396

Query Match 7.5%; Score 76; DB 4; Length 376;
Best Local Similarity 26.8%; Pred. No. 3.4;
Matches 37; Conservative 12; Mismatches 49; Indels 40; Gaps 7;

QY 4 AVGRRWAAALLLAAVAVLTVV-----MLW---LGTQSFVQREEE----- 41
Db 237 APGRPWYLLLVAAVPAALLLLAVGVGLLRPELHAPAWLWQFILLANLFFVSLAEEALFRGY 296
QY 42 IAQLARQYAGLDHELAFSRLIVELRRLHPGHVLPDEELQWVFVNAGG-----WMGAM 93
Db 297 LQORLGQWLGWPALALASALFGLAHFAGGPLL-----MLFAGLAGLIYGLAWLWSGRL 350
QY 94 ---CLLHASLS-EYVLLF 107
Db 351 WATLPHFGLNLTHLLLF 368

Search completed: October 29, 2005, 04:51:36
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:38:34 ; Search time 168 Seconds
(without alignments)
477.763 Million cell updates/sec

Title: US-09-823-069A-2
Perfect score: 1016
Sequence: 1 MQWAGRRWAAALLAVAA.....RSVARGRLRLTYLFGQDP 192

Scoring table: BLOSUM62

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Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10G_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1016	100.0	192	9	US-09-823-069-2
2	925	91.0	192	9	US-09-823-069-4
3	827.5	81.4	195	9	US-09-925-298-455
4	827.5	81.4	195	14	US-10-102-806-455
5	212.5	20.9	222	15	US-10-369-493-1902
6	206	20.3	219	15	US-10-369-493-2143
7	204	20.1	285	15	US-10-369-493-4103
8	180	17.7	429	15	US-10-369-493-13403
9	86	8.5	421	16	US-10-437-963-118957
10	85	8.5	471	16	US-10-481-265-93
11	85.5	8.4	335	14	US-10-156-761-12590

12	85	8.4	307	14	US-10-156-761-14148	Sequence 14148, A
13	83	8.2	1158	9	US-09-834-792-2	Sequence 2, Appli
14	83	8.2	1158	13	US-10-026-188-5	Sequence 5, Appli
15	83	8.2	1158	16	US-10-794-897-4	Sequence 4, Appli
16	81.5	8.0	440	15	US-10-282-122A-61930	Sequence 61930, A
17	81.5	8.0	523	15	US-10-369-493-12888	Sequence 12888, A
18	81	8.0	352	16	US-10-437-963-137218	Sequence 137218, A
19	81	8.0	630	15	US-10-405-877-43	Sequence 43, Appli
20	81	8.0	840	14	US-10-156-761-13027	Sequence 13027, A
21	80.5	7.9	354	15	US-10-424-599-279814	Sequence 279814, A
22	80.5	7.9	361	15	US-10-425-114-46329	Sequence 46329, A
23	80	7.9	527	17	US-10-732-923-4147	Sequence 4147, Ap
24	79.5	7.8	363	15	US-10-425-114-72368	Sequence 72368, A
25	79.5	7.8	491	15	US-10-282-122A-78405	Sequence 78405, A
26	79.5	7.8	512	16	US-10-437-963-184765	Sequence 184765, A
27	79.5	7.8	1926	16	US-10-437-963-132922	Sequence 132922, A
28	79	7.8	330	14	US-10-221-087-43	Sequence 43, Appli
29	78.5	7.7	469	15	US-10-369-493-16951	Sequence 16951, A
30	78	7.7	436	16	US-10-437-963-196797	Sequence 196797, A
31	78	7.7	1035	15	US-10-282-122A-51321	Sequence 51321, A
32	77.5	7.6	231	16	US-10-425-115-228673	Sequence 228673, A
33	77	7.6	273	17	US-10-732-923-15741	Sequence 15741, A
34	77	7.6	400	16	US-10-437-963-169852	Sequence 169852, A
35	77	7.6	439	9	US-09-967-477B-4	Sequence 4, Appli
36	77	7.6	595	16	US-10-437-963-129532	Sequence 129532, A
37	77	7.6	944	14	US-10-213-990-27	Sequence 27, Appli
38	77	7.6	1168	16	US-10-794-897-8	Sequence 8, Appli
39	76.5	7.5	479	14	US-10-156-761-8209	Sequence 8209, Ap
40	76	7.5	99	16	US-10-425-115-35924	Sequence 35924, A
41	76	7.5	193	16	US-10-767-701-33261	Sequence 33261, A
42	76	7.5	392	18	US-10-450-763-37569	Sequence 37569, A
43	76	7.5	473	14	US-10-156-761-12103	Sequence 12103, A
44	75.5	7.4	470	17	US-10-732-923-23727	Sequence 23727, A
45	75.5	7.4	690	20	US-11-097-143-16488	Sequence 16488, A

ALIGNMENTS

RESULT 1
US-09-823-069-2
; Sequence 2, Application US/09823069
; Patent No. US20020061847A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Kenneth
; APPLICANT: Mach, Robert
; APPLICANT: Childers, Steven
; APPLICANT: Shelness, Gregory
; APPLICANT: Wang, Li-Ming
; TITLE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE VARIANT
; FILE REFERENCE: 9151.6
; CURRENT APPLICATION NUMBER: US/09/823,069
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,694
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-069-2

Query Match 100.0%; Score 1016; DB 9; Length 192;
Best Local Similarity 100.0%; Pred. No. 7.2e-99;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQWAGRRWAAALLAVAAVLTVQVWLWLGTSFVQREIIAQLARQYAGLDHDLAFSR 60
DB 1 MQWAGRRWAAALLAVAAVLTVQVWLWLGTSFVQREIIAQLARQYAGLDHDLAFSR 60
QY 61 LIVELRLHPGHVLPDEELQWVFVNAGWGMGMCLLHSLSEYVLLFGTALGSRGHSGET 120

```
Db 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSSEYVLLFGTALGSRGSGT 120
Qy 121 VVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 180
Db 121 VVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 180
Qy 181 LELTTYLFGQDP 192
Db 181 LELTTYLFGQDP 192

RESULT 2
US-09-823-069-4
; Sequence 4, Application US/09823069
; Patent No. US20020061847A1
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Kenneth
; APPLICANT: Mach, Robert
; APPLICANT: Childers, Steven
; APPLICANT: Shelness, Gregory
; APPLICANT: Wang, Li-Ming
; TITLE OF INVENTION: METHODS AND COMPOSITIONS UTILIZING AN ALTERNATIVE SPLICE VARIANT
; TITLE OF INVENTION: SIGMA-1 RECEPTOR
; FILE REFERENCE: 9151.6
; CURRENT APPLICATION NUMBER: US/09/823,069
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,694
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-823-069-4

Query Match 91.0%; Score 925; DB 9; Length 192;
Best Local Similarity 89.0%; Pred. No. 3e-89;
Matches 170; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MWAGRRWAWALILAVAVLTQVVLWLTQSFVFOREEIAQLARQYAGLDHELAFSR 60
Db 1 MPWAGRRWAWTLITITIAVLIQAALWLTQNFVFSREEIAQLARQYAGLDHELAFSR 60
Qy 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSSEYVLLFGTALGSRGSGT 120
Db 61 LIVELRLHPGHVLPDEELQWVFNAGGWMGAMCLLHASLSSEYVLLFGTALGSRGSGT 120
Qy 121 VVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 180
Db 121 VVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 180
Qy 181 LELTTYLFGQD 191
Db 181 LELTTYLFGQD 191

RESULT 3
US-09-925-298-455
; Sequence 455, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
```

```
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-455

Query Match 81.4%; Score 827.5; DB 9; Length 195;
Best Local Similarity 83.9%; Pred. No. 6e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 31 GTQSFVFOREEIAQLARQYAGLDHELAFSRLIVELRRLHPGHVLPDEELQWVFNAGGWM 90
Db 3 GTQSFVFOREEIAQLARQYAGLDHELAFSRLIVELRRLHPGHVLPDEELQWVFNAGGWM 62
Qy 91 GAMCLLHASLSSEYVLLFGTALGSRGHS-----GE 119
Db 63 GAMCLLHASLSSEYVLLFGTALGSRGHSRYWAEISDTIISGTFHQWREGTTKSEVFPGE 122
Qy 120 TVVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 179
Db 123 TVVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 182
Qy 180 RLETTYLFGQDP 192
Db 183 RLETTYLFGQDP 195

RESULT 4
US-10-102-806-455
; Sequence 455, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 455
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-455

Query Match 81.4%; Score 827.5; DB 14; Length 195;
Best Local Similarity 83.9%; Pred. No. 6e-79;
Matches 162; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy 31 GTQSFVFOREEIAQLARQYAGLDHELAFSRLIVELRRLHPGHVLPDEELQWVFNAGGWM 90
Db 3 GTQSFVFOREEIAQLARQYAGLDHELAFSRLIVELRRLHPGHVLPDEELQWVFNAGGWM 62
Qy 91 GAMCLLHASLSSEYVLLFGTALGSRGHS-----GE 119
Db 63 GAMCLLHASLSSEYVLLFGTALGSRGHSRYWAEISDTIISGTFHQWREGTTKSEVFPGE 122
Qy 120 TVVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 179
Db 123 TVVHGPGEATAVWGPNMTVMVEYGRGVIPSTLAFALADTVFSTQDFLTLYTLRSYARGLR 182
Qy 180 RLETTYLFGQDP 192
Db 183 RLETTYLFGQDP 195
```



```
; SEQ ID NO 12590
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12590

Query Match      8.4%; Score 85.5; DB 14; Length 335;
Best Local Similarity 26.0%; Pred. No. 2.8;
Matches 58; Conservative 23; Mismatches 81; Indels 61; Gaps 14;

QY 9 WAAALLLAAVAVLTQVWMLGT-----QSFVQREIEIAQLARQYAGLDHDLAFSLIVE 64
DB 103 WPTALLSTVAVL--LGM-WIGTHPEVQSSIAAPSELRALTR--PGGEYETVYSS----- 153
QY 65 LRLHPLGHVLPDEELQWVFNAGGWMGAMCLLHA-----SLSEYVLLFCTALGSRG 115
DB 154 ----HPAASFAAQ-----VMTN-NAQAAMCLVIGFLGFLVILFQNNMLNLGVGLGMS 204
QY 116 HSQE-----TVVHGPGEATAV-----EW-----GP-----NTMWVEYGRGVIPST 150
DB 205 SAGRLDTFGLVLPGLHLELTAVFVAGTCLRLGWLIDPGPSPRRTALAEGRALGWA 264
QY 151 LAPALADTVFSTQDFTLFLFYLRSYAR---GLRLELT--TYLP 188
DB 265 VGLALVLFVSGAIEGFVTPSGLPTWARIGIGIAAELAFITYY 307

RESULT 12
US-10-156-761-14148
; Sequence 14148, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 14148
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-14148

Query Match      8.4%; Score 85; DB 14; Length 307;
Best Local Similarity 26.2%; Pred. No. 2.9;
Matches 51; Conservative 24; Mismatches 62; Indels 58; Gaps 9;

QY 14 LLLAAVAVLTQVWMLGTQSFVQREIEIAQLARQYAGLDHDLAFSLIVELRLHPGHV 73
DB 16 LVLAVSNAFC---LGIG---FVLQ-----QNAQAHPALSDFLS-PRLLLDLMHVR----- 58
QY 74 LPDEELQW----FVNAGGWMGAMCLLHASLSEYVLLFGT-----ALGSR 114
DB 59 -----RWLGGIGFVWVGVGLAVALAHGELSILVEPLLATNLLFALGSLSRQTKQPLGRQ 112
QY 115 GHSGETVWHPGEATAVENGP-----NTMWVEYGRGVIPSTLAPALADTVFSTQD 164
DB 113 GWAGLALLAGGVTAFTVAGQPTGGDAVTNPLRHWV-----IIGVMVGFALLLTTAKQS 166
QY 165 FLTLFVTLRSYARGL 179
DB 167 RLSAAPVLLSLAAGL 181

RESULT 13
US-09-834-792-2
; Sequence 2, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; TITLE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165.0589
; CURRENT APPLICATION NUMBER: US/09/834,792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Murine TRP8
US-09-834-792-2

Query Match      8.2%; Score 83; DB 9; Length 1158;
Best Local Similarity 22.2%; Pred. No. 25;
Matches 40; Conservative 17; Mismatches 53; Indels 70; Gaps 7;

QY 29 WLGTQSF-VFQREIEIAQLARQYAGLDHDLAFSLIVEL-----RRLH----- 69
DB 102 WILTSALHVLARHVQAVR-----DHSLASTSTKIRVVAIGMASLDRLHROLLDGVHQ 156
QY 70 ----PGHVLPEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALGS----- 113
DB 157 KEDTPIHYPADE-----GNIQGPLCLDSNLSHFILVESGALSGNDGLTELQLSL 207
QY 114 -----RGHSGETVWHPGEATAVENGPNT-----NMVEYGRGVIPSTLA 152
DB 208 EXHISQRTGYGTCIQIPVLCLLVNGDPNTILERSRAVEQAAPWLLLAGSGGIADVLA 267

RESULT 14
US-10-026-188-5
; Sequence 5, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence
US-10-026-188-5

Query Match      8.2%; Score 83; DB 13; Length 1158;
Best Local Similarity 22.2%; Pred. No. 25;
Matches 40; Conservative 17; Mismatches 53; Indels 70; Gaps 7;

QY 29 WLGTQSF-VFQREIEIAQLARQYAGLDHDLAFSLIVEL-----RRLH----- 69
DB 102 WILTSALHVLARHVQAVR-----DHSLASTSTKIRVVAIGMASLDRLHROLLDGVHQ 156
```

QY 70 -----PCHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALGS----- 113
Db 157 KEDTPIHYPADE-----GNIQGPLCLDSNLSHFILVESGALSGNDGLTELQLSL 207
QY 114 -----RGHSGETVVGHPGEATAVEMGPNT-----WMVEYGRGVIPSTILA 152
Db 208 EXHISQORTGYGTSIQIPVLCLLVNGDPNTLERISRAVEQAAPWLLAGSGGIADVLA 267

RESULT 15
US-10-794-897-4
; Sequence 4, Application US/10794897
; Publication No. US20040259160A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Zhou, Yun-Ping
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes and Related Diseases Involving Beta-TRP
; FILE REFERENCE: 016325-019010US
; CURRENT APPLICATION NUMBER: US/10/794,897
; PRIOR FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: US 60/452,596
; PRIOR FILING DATE: 2003-03-05
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse betaTRP (TRPM5) calcium channel
US-10-794-897-4

Query Match 8.2%; Score 83; DB 16; Length 1158;
Best Local Similarity 22.2%; Pred. No. 25;
Matches 40; Conservative 17; Mismatches 53; Indels 70; Gaps 7;
QY 29 WLGTQSF-VFQREETIAQLARQVAGLDHDLAFSRLVEL-----RRLH----- 69
Db 102 WILTSALHVGARHVGQAVR-----DHSLASTSTKIRVVAIGMASLDRILHRQLLDGVHQ 156
QY 70 -----PCHVLPDEELQWVFNAGGWMGAMCLLHASLSEYVLLFGTALGS----- 113
Db 157 KEDTPIHYPADE-----GNIQGPLCLDSNLSHFILVESGALSGNDGLTELQLSL 207
QY 114 -----RGHSGETVVGHPGEATAVEMGPNT-----WMVEYGRGVIPSTILA 152
Db 208 EXHISQORTGYGTSIQIPVLCLLVNGDPNTLERISRAVEQAAPWLLAGSGGIADVLA 267

Search completed: October 29, 2005, 04:50:48
Job time : 170 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 29, 2005, 04:37:06 ; Search time 39 seconds
(without alignments)
473.683 Million cell updates/sec

Title: US-09-823-069A-2
Perfect score: 1016
Sequence: 1 MQWAVGRRWAAALLAVAA.....RSVAGRLDELTYLFGQDP 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: Pirl2:.*
3: Pirl3:.*
4: Pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	990.5	97.5	223	JC5266	sigma receptor 1 -
2	903.5	88.9	223	JC5815	sigma receptor 1 -
3	226.5	22.3	256	T46871	C-8 sterol isomera
4	212.5	20.9	222	JH0488	C-8 sterol isomera
5	210.5	20.7	221	S33457	C-8 sterol isomera
6	206	20.3	219	T38129	C-8 sterol isomera
7	183.5	18.1	241	S29697	C-8 sterol isomera
8	94	9.3	393	B86189	protein T2SN20.9 [
9	86	8.5	471	H70559	hypothetical prote
10	84	8.3	382	D75541	probable CynX-rela
11	83	8.2	401	YTECT0	tetracycline resis
12	83	8.2	644	T34879	probable integral
13	83	8.2	789	C83949	hypothetical prote
14	81.5	8.0	253	AF2310	serine acetyltrans
15	81.5	8.0	345	H86150	hypothetical prote
16	81.5	8.0	1198	T28678	polyketide synthas
17	81	8.0	385	E83506	probable MFS trans
18	80.5	7.9	460	T09956	NADH2 dehydrogenas
19	80	7.9	121	AC2869	conserved hypotcet
20	80	7.9	121	E97645	hypothetical prote
21	80	7.9	415	AG2044	hypothetical prote
22	80	7.9	597	B55513	hoxx protein - Alc
23	79.5	7.8	178	A69450	anthranilate synth
24	79.5	7.8	491	AH0345	probable divalent
25	79.5	7.8	692	S37976	hypothetical prote
26	79	7.8	629	T36473	probable sodium/pr
27	78.5	7.7	250	A11981	serine acetyltrans
28	78.5	7.7	431	E82139	hypothetical prote
29	78.5	7.7	460	T09866	NADH2 dehydrogenas

30	78.5	7.7	469	2	G87513	beta-glucosidase [
31	78	7.7	1159	2	E70741	probable regulator
32	77.5	7.6	548	2	G70610	hypothetical prote
33	77	7.6	216	2	F69166	hypothetical prote
34	77	7.6	459	2	S10196	NADH2 dehydrogenas
35	77	7.6	527	2	AE2932	Na+/H+ antiporter
36	77	7.6	550	2	B98350	hypothetical prote
37	76.5	7.5	324	2	G69851	conserved hypotcet
38	76.5	7.5	339	2	T29057	hypothetical prote
39	76.5	7.5	410	2	C84176	oxalate/formate an
40	76.5	7.5	471	2	AC3450	Na+ driven multidr
41	76	7.5	272	2	H83004	hypothetical prote
42	76	7.5	689	2	AD0336	conserved hypotcet
43	75.5	7.4	262	2	G82280	vibriobactin-speci
44	75.5	7.4	507	2	S76687	hypothetical prote
45	75	7.4	275	2	S77462	hypothetical prote

ALIGNMENTS

RESULT 1

JC5266

sigma receptor 1 - human

C;Species: Homo sapiens (man)

C;Date: 25-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004

C;Accession: JC5266

R;Kekuda, R.; Prasad, P.D.; Rei, Y.J.; Leibach, F.H.; Ganapathy, V.

Biochem. Biophys. Res. Commun. 229, 553-558, 1996

A;Title: Cloning and functional expression of the human type 1 sigma receptor (hsigmaR1)

A;Reference number: JC5266; MUID:97127440; PMID:8954936

A;Contents: placental cell

A;Accession: JC5266

A;Molecule type: mRNA

A;Residues: 1-223 <KEK>

A;Cross-references: UNIPROT:Q99720; GB:U75283; NID:g1906590; PIDN:AB50402.1; PID:g1783

C;Comment: This receptor interacts with several antipsychotic drugs such as haloperidol

F;92-113/Domain: transmembrane #status predicted <TMM>

Query Match 97.5%; Score 990.5; DB 2; Length 223;

Best Local Similarity 86.1%; Pred. No. 1.5e-85;

Matches 192; Conservative 0; Mismatches 0; Indels 31; Gaps 1;

Qy	1	MQWAVGRRWAAALLAVAAVLTVVWLMLGTQSFVQREIEIAQLARQYAGLDHDLAFSR	60
Db	1	MQWAVGRRWAAALLAVAAVLTVVWLMLGTQSFVQREIEIAQLARQYAGLDHDLAFSR	60
Qy	61	LIVELRLHPGHVLPDEELQWVFVNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHS---	117
Db	61	LIVELRLHPGHVLPDEELQWVFVNAGWGMGAMCLLHASLSEYVLLFGTALGSRGHSRY	120
Qy	118	-----GFTVVHGCEATAVEMGPNMTWVEYGRGVIPS	149
Db	121	WAFISDTIISGTFHQWREGTKSEVYPGTFVHGPGCEATAVEMGPNMTWVEYGRGVIPS	180
Qy	150	TLAFALADTVFSTQDFLTFLTYLRSYARGLRLELTLYLFCQDP	192
Db	181	TLAFALADTVFSTQDFLTFLTYLRSYARGLRLELTLYLFCQDP	223

RESULT 2

JC5815

sigma receptor 1 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 09-Jul-2004

C;Accession: JC5815

R;Seth, P.; Leibach, F.H.; Ganapathy, V.

Biochem. Biophys. Res. Commun. 241, 535-540, 1997

A;Title: Cloning and structural analysis of the cDNA and the gene encoding the murine t

A;Reference number: JC5815; MUID:98086386; PMID:9425306

A;Accession: JC5815

A;Molecule type: mRNA

A;Residues: 1-223 <SET>

A:Cross-references: UNIPROT:055242; GB:AF030198; NID:g2809119; PIDN:AAC39951.1; PID:g2809119
C:Comment: This protein interacts with endogenous steroid hormones, progesterone and testosterone
C:Genetics: 51/1; 118/1; 149/1
A:Introns: 171; Domain: transmembrane #status predicted <TMM>

Query Match 88.9%; Score 903.5; DB 2; Length 223;
Best Local Similarity 77.0%; Pred. No. 2.2e-77;
Matches 171; Conservative 7; Mismatches 13; Indels 31; Gaps 1;

QY 1 MQWAVGRRWAAALLIAVAALVTQVVMWLGTSQVFQREIEIAQLARQYAGLDHSLAFS 60
DB 1 MPWAGRRWAWITLITIAVLIAQAWLWLTQNFVFSREIEIAQLARQYAGLDHSLAFS 60
QY 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALSGRHS --- 117
DB 61 LIVELRLHPGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALSGHSGRY 120
QY 118 -----GETVVHGPGEATAVEMGPNMTVMVYGRGVIPS 149
DB 121 WAEISDTISGTHQWKEGTTKSEVPYGETVVHGPGEATALEWGNMTVMVYGRGVIPS 180
QY 150 TLAFALADTVFSTQDFTLTYLRSYARGLRLELTLYLFGQD 191
DB 181 TLFFALADTVFSTQDFTLTYLRSYARGLRLELTLYLFGQD 222

RESULT 3
T46871
N:Alternate names: EC 5.3.3.- [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C:Accession: T46871
R:Gilbert, J.; Orbach, M.J.
submitted to the EMBL Data Library, May 1996
A:Reference number: Z24117
A:Accession: T46871
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-256 <GIL>
A:Cross-references: UNIPROT:092254; EMBL:U59671; PIDN:AAB09470.1
A:Experimental source: strain OR23-74-1A
C:Genetics:
A:Gene: erg-1
A:Map position: V
A:Introns: 145/1
C:Keywords: intramolecular oxidoreductase; isomerase; sterol biosynthesis

Query Match 22.3%; Score 226.5; DB 2; Length 256;
Best Local Similarity 33.7%; Pred. No. 8.6e-14;
Matches 69; Conservative 33; Mismatches 62; Indels 41; Gaps 7;

QY 4 AVGRRWAAALLIAVAALVTQVVMWLGTSQVFQREIEIAQLARQYAGLDHSLAFS 59
DB 39 SIGGWUKFPAIPALVAPAYVLEQRL--ESFVFDTEHLHLDSKRAISRSHGNDTKAIVK 96
QY 60 RLIVEL--RLRHGHVLPDEELQWVFNAGWGMGAMCLLHASLSEYVLLFGTALSGRHS 117
DB 97 YIVDELNDNGVAPYNNDEE--WVFNAGGAGMAYIIHASITEVLIIFGTAGTEGHT 154
QY 118 G-----ETVVHGPGEATAVEMGPNMTVMVYGRGVIPS 146
DB 155 GRHTADDYFHLTGTQTVVPGGEYEPVPGSVVHVLVRGTVKQYRMPESCFALEYPRGW 214
QY 147 IPSTLAFALADTVFSTQDFTLTYLRSYARGLRLELTLYLFGQD 171
DB 215 IPMLFFGYADTVLSTLSDFTLWRT 239

RESULT 4
JH0488
C-8 sterol isomerase - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein YM8325.03; protein YMR202w
C:Species: Saccharomyces cerevisiae
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: JH0488; S59443
R:Arthington, B.A.; Hoskins, J.A.; Skatrud, P.L.; Bard, M.
Gene 107, 173-174, 1991
A:Title: Nucleotide sequence of the gene encoding yeast C-8 sterol isomerase.
A:Reference number: JH0488; MUID:92077431; PMID:1743517
A:Accession: JH0488
A:Molecule type: DNA
A:Residues: 1-222 <ART>
A:Cross-references: UNIPROT:P32352; EMBL:M74037; NID:g171472; PIDN:AAA34593.1; PID:g171472
R:Odell, C.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A:Reference number: S59441
A:Accession: S59443
A:Molecule type: DNA
A:Residues: 1-222 <ODR>
A:Cross-references: EMBL:Z48755; NID:g736296; PIDN:CAA88643.1; PID:g736299; MIPS:YMR202w
A:Experimental source: strain AB972
C:Comment: This enzyme catalyzes the reaction which results in unsaturation at C-7 in the
C:Genetics:
A:Gene: SGD:ERG2
A:Cross-references: SGD:S0004815; MIPS:YMR202w
A:Map position: 13R
C:Keywords: transmembrane protein
F:6-12/Domain: transmembrane #status predicted <TMM>

Query Match 20.9%; Score 212.5; DB 2; Length 222;
Best Local Similarity 30.0%; Pred. No. 1.5e-12;
Matches 62; Conservative 36; Mismatches 66; Indels 43; Gaps 8;
QY 14 LLLAAVAALVTQVVMWLGTSQVFQREIEIAQLARQYAGLDHE---LAFSRLIVELRLH 69
DB 8 LLIGVGVYIMNVLTFTLPT-NYMPDPKPTLANEICNSVISKHNABEGLSTEDLLQDVDRAL 66
QY 70 PGHVLDPDEL-----QWVFNAGWGMGAMCLLHASLSEYVLLFGTALSGRHSGE --- 119
DB 67 ASH-YGDEYINRYKVEWVFNAGWGMGAMCLLHASVSEYLLIFGTAVGTEGHTGVHPAD 125
QY 120 ---TVVHG-----PGEATAVEMGPNMTVMVYGRGVIPSTLTA 152
DB 126 DVFTILHGTQIAALPYATEAEVYTPGMTHLKKGYAKQVMPGSGFALELAQCWIPCMPL 185
QY 153 FALADTVFSTQDFTLTYLRSYARGLR 179
DB 186 FGFLDTFSSTLDTLYTFTVYLTARDM 212

RESULT 5
S33457
C-8 sterol isomerase - rice blast fungus
C:Species: Magnaporthe grisea (rice blast fungus)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S44061; S33457
R:Keon, J.P.R.; James, C.S.; Court, S.; Baden-Daintree, C.; Bailey, A.M.; Burden, R.S.;
Curr. Genet. 25, 531-537, 1994
A:Title: Isolation of the ERG2 gene, encoding sterol Delta(8) -> Delta(7) isomerase, fr
A:Reference number: S44061; MUID:94363780; PMID:8082205
A:Accession: S44061
A:Molecule type: DNA
A:Residues: 1-221 <KE2>
A:Cross-references: UNIPROT:P33281; EMBL:Z22775; NID:g311321; PID:g311322
C:Genetics:
A:Introns: 101/1

Query Match 20.7%; Score 210.5; DB 2; Length 221;
Best Local Similarity 30.2%; Pred. No. 2.3e-12;
Matches 60; Conservative 31; Mismatches 65; Indels 43; Gaps 5;
QY 11 WAALLAAVAALVTQVVMWLGTSQ---FVFOREIEIAQLARQ---YAGLDHSLAFSRLIV 63
DB 11 FVAVLLAAVVSPL-----VYLAERLESFYVFDHKLHSLSTQIAIAQHGNNTAIVGHIVD 65

A:Authors: Sqaes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: H70559

C:Species: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-471 <COL>

A:Cross-references: UNIPROT:O06151; GB:295554; GB:AL123456; NID:g3261771; PIDN:CA808887.

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: Rv1634

C:Superfamily: tetracycline resistance protein

Query Match 8.5%; Score 86; DB 2; Length 471;
Best Local Similarity 25.3%; Pred. No. 2.6;
Matches 41; Conservative 18; Mismatches 55; Indels 48; Gaps 8;

QY 9 WAWA---ALLAVAAVLTQV-----RRLLH-----PGHVLDPDEELQWVFNAGWMG 91
DB 172 WNAFGVWTLTALWMLVPVVALGAGVGGGETPVGTHKVPVWSLLMGAALAI SVA 231

QY 41 ETIAQLARQVAGLDHSLFSLVEL-----RRLLH-----PGHVLDPDEELQWVFNAGWMG 91
DB 232 ALPNVILVQTAGL---LAAALLVAVFVVVDWRIHAAVLPPSVFGSGPLKWIYLTW----- 283

QY 92 ANCLLHASLSEYVLLFGTALSGRHSGETTVVHGPGEATAVEW 133

DB 284 SVQMTAAWVDVTVPLFGQRL---GHLTPVAGFLGAALAVGW 322

RESULT 10
D75541
probable CynX-related transport protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: D75541
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioreistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75541
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <WHI>
A:Cross-references: UNIPROT:O9RXP9; GB:AE001887; GB:AE000513; NID:g6457928; PIDN:AAF0984
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0260
A:Map position: 1
C:Superfamily: cynX protein

Query Match 8.3%; Score 84; DB 2; Length 382;

Best Local Similarity 32.9%; Pred. No. 3.2;

Matches 49; Conservative 10; Mismatches 38; Indels 52; Gaps 9;

QY 9 WAW---AALLAVAAVL-----TQVVMMLMGTSFVFQREETAQ 44
DB 167 WAWLSGAALLAWPAMLGPARSAGPAVRGSPVWSNPATLPVTLYMGTSQSLVF-FWLWTW 225

QY 45 LAR-QYAGLDHSLFSLVEL-----RRLLHGHVLPDEELQWVFNAGWMG 84
DB 226 LARLLQDRGLSAAAGALLSLGNLVLQPLTSLVPVLSRL--GNVRP-----LVFGLVAC 278

QY 85 NAGGWMGAMCLLHASLSEYVLLFGTALSG 113
DB 279 NAAGLLGLTLWPTASPPLPWLLLVGAGS 307

RESULT 11
YBCT0
tetracycline resistance protein - Escherichia coli transposon Tn10

C:Species: Escherichia coli
C:Date: 13-Jun-1983 #sequence_revision 20-Sep-1984 #text_change 09-Jul-2004
C:Accession: A91505; A93481; A03507
R:Nguyen, T.T.; Postle, K.; Berstrand, K.P.
Gene 25, 83-92, 1983

A:Title: Sequence homology between the tetracycline-resistance determinants of Tn10 and

A:Reference number: A91505; MUID:84109550; PMID:6319234

A:Accession: A91505

A:Molecule type: DNA

A:Residues: 1-401 <NGU>

A:Cross-references: UNIPROT:P02980

R:Hillen, W.; Schollmeier, K.

Nucleic Acids Res. 11, 525-539, 1983

A:Title: Nucleotide sequence of the Tn10 encoded tetracycline resistance gene.

A:Reference number: A93481; MUID:83143319; PMID:6298728

A:Accession: A93481

A:Molecule type: DNA

A:Residues: 1-280, 'E', 282-300, 'D', 302-329, 'E', 331-353, 'T', 355-401 <HL>

A:Cross-references: GB:V00611; NID:g43700; PIDN:CAA23880.1; PID:g43701

C:Genetics:

A:Gene: tet

C:Superfamily: tetracycline resistance protein

C:Keywords: antibiotic resistance; transmembrane protein

Query Match 8.2%; Score 83; DB 1; Length 401;
Best Local Similarity 29.2%; Pred. No. 4.2;
Matches 38; Conservative 18; Mismatches 42; Indels 32; Gaps 7;

QY 14 LLLAAVAVLTQVVMMLGTSFVFQREETAQLARQVAGLDH-ELAFSRLI--VELRRLHP 70
DB 45 VLLALYALMVQIFAPWLGKMSDRGRRPRLVLLSLIGASLDVLLAFSSALWMLYLGRLLS 104

QY 71 G-----HVLDP-----BELOWFVNAGWMGAMCLLHASLSEYVLLFGTALSGRG 115
DB 105 GITCATCAVAASVIADTTTSASQVKWF-----GMLGASFGLG-----LIAGPIIG--G 150

QY 116 HSGETVVHGP 125

DB 151 FAGEISPHSP 160

RESULT 12
T34879
probable integral membrane protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T34879
R:Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z21561
A:Accession: T34879
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-644 <OLI>
A:Cross-references: UNIPROT:O69917; EMBL:AL023861; PIDN:CAA19596.1; GSPDB:GN00070; SCORI
C:Genetics:
A:Gene: SCORDB:SC3C8.04c

Query Match 8.2%; Score 83; DB 2; Length 644;
Best Local Similarity 26.9%; Pred. No. 7.3;
Matches 46; Conservative 18; Mismatches 63; Indels 44; Gaps 9;

QY 12 AALLAAVAVLTQVVMMLGTSFVFQREETAQL-ARQVAGLDH-ELAFSRLIIVELRRLH 69
DB 110 AAVALLVDYVTVAVQVSAGTSALV-----SLAHLVGNWGTGLDHLQVPVSLVIVL--LG 163

QY 70 PGHVLDPDEELQWVFNAGWMGAMCLLHASLSEYVLLFGTALSGRHSGETTVVHGPGREAT 129
DB 164 YGNLRGVRE-----AGRMFALPAYLFAAAMGLVFLVAAVRGLRGELPHADLHAPG---- 213

QY 130 AVEWGP--NTWVVEYGRGVIPSTLAFALADTVFSTQDFLFTFYTLRSVARG 178

Db 214 VPLGTPGDGWL--YG-----ASLFIVLRSFANG 240

RESULT 13

C83949

hypothetical protein spoIIIE [imported] - Bacillus halodurans (strain C-125)

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: C83949

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: C83949

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-789 <STO>

A;Cross-references: UNIPROT:Q9KA95; GB:AP001515; GB:BA000004; NID:gl0174886; PIDN:BA0601

A;Experimental source: strain C-125

C;Genetics:

A;Gene: spoIIIE

C;Superfamily: Bacillus subtilis DNA translocase spoIIIE

Query Match 8.2%; Score 83; DB 2; Length 789;

Best Local Similarity 27.0%; Pred. No. 9.2;

Matches 57; Conservative 25; Mismatches 69; Indels 60; Gaps 12;

QY 7 RRWAWAA-----LLAVANVLTQVVMWLTQSFVFOREIAQLARQYAGLDHE 55

Db 8 KKVAMQSQLTPELVGLVIAVVA-LAQ-----LGTVGSTLVRLFRFFLGEWYAVLSIA 61

QY 56 LAFSLVIVLRLHPGHVLPDEELQWVFNAGWGMAMCLLHASLSEYVLLFGTALGSRG 115

Db 62 LLVAALYIWMRKPP-----LW-SRRIGLY--LMLLSALLSHVGLFQLOGNEG 110

QY 116 HSGETVVHGPGEATAVEMGNTWMV-----EYGRVIPSTLAFALADTVFSTQ 163

Db 111 FSPQSVIR-----NTNLFWLDWYGEVQSHDLGGMI-GAIAVAASHFLFA-- 155

QY 164 DFLTLFTLRSYARGLRLELT-----TVLFQ 190

Db 156 DGGTLCFLCFILFMAGLIL-LTGHISITDLFGK 185

RESULT 14

AF2310

serine acetyltransferase [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AF2310

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AF2310

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-253 <KUR>

A;Cross-references: UNIPROT:Q8YQ03; GB:BA000019; PIDN:BAB75736.1; PID:gl7133172; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: all4037

C;Superfamily: Bacillus serine acetyltransferase; serine acetyltransferase homology

Query Match 8.0%; Score 81.5; DB 2; Length 253;

Best Local Similarity 25.0%; Pred. No. 3.4;

Matches 32; Conservative 19; Mismatches 34; Indels 43; Gaps 6;

QY 22 LTVQVLMWLTQSFVFOR-----BEIAQLARQYAGLDHDLAFSRLIVELRR 67

Db 22 LLEVLFCYCGUQLLHFRVNWLYRLGLPIPLRIISHARFLTGIE----- 67

QY 68 LHPGHVLPDEELQWVFNAGWGMAMCLLHASLSEYVLLF-GPALSGRHS-----G 118

Db 68 IHPGATIG---QGVFIDHG--MGVVIGETAIVGDYVALIYQGVTLGGTGKSGKRHPITLG 121

QY 119 ETVVHGPG 126

Db 122 ENVVVGAG 129

RESULT 15

H86150

hypothetical protein F22M8.4 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C;Accession: H86150

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso

Chin, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: H86150

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <STO>

A;Cross-references: UNIPROT:Q9LPD0; GB:AE005172; NID:g8570442; PIDN:AAF76469.1; GSPDB:G

C;Genetics:

A;Map position: 1

C;Superfamily: arsenical pump-driving ATPase

Query Match 8.0%; Score 81.5; DB 2; Length 345;

Best Local Similarity 24.8%; Pred. No. 4.9;

Matches 35; Conservative 16; Mismatches 57; Indels 33; Gaps 5;

Search completed: October 29, 2005, 04:48:01

Job time : 49 secs

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